



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 171411

TO: Minh-Tam Davis
Location: REM-3A24&3C18
Art Unit: 1642
Wednesday, November 16, 2005
Case Serial Number: 09/856812

From: Barb O'Bryen
Location: Biotech-Chem Library
Remsen 1a69
Phone: 571-272-2518 *BOB*

barbara.obryen@uspto.gov

Search Notes

THIS PAGE BLANK (USPTO)

STIC-Biotech/ChemLib

141411

From: Davis, Minh-Tam
Sent: Monday, November 14, 2005 11:47 AM
To: STIC-Biotech/ChemLib
Subject: Search request for 09/856812

Please search in commercial database, issued patent files, PGPUB:

- 1) SEQ ID NO: 42 with and without size limitation for the sequences in the database to the size of the sequence.
- 2) SEQ ID NO:1

Thank you.

MINH TAM DAVIS

ART UNIT 1642, ROOM 3A24, MB 3C18

272-0830

CRFE

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: 11/16/05
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIS: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

73622

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 15, 2005, 15:28:51 ; Search time 233.31 Seconds
(without alignments)
611.696 Million cell updates/sec

Title: US-09-856-812b-1
Perfect score: 1891
Sequence: 1 MPRAPRQRQMPEDLQSQS.....DTTAMASASSATGFSFYPE 369

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB ID	Description
1	1891	100.0	369	3 AAY71485	Aay71485 Human MAG
2	1891	100.0	369	4 AAB80297	Aab80297 Human pro
3	1891	100.0	369	6 ABR48215	Abr48215 Human bla
4	1891	100.0	369	6 ABU56516	Abu56516 Lung canc
5	1852	97.9	383	8 ABO58424	Abos8424 Human gen
6	911	48.2	394	8 ADR09600	Adr09600 Human pro
7	911	48.2	429	3 AAB08736	Aab08736 Amino aci
8	910	48.1	318	3 AAB08734	Aab08734 Amino aci
9	910	48.1	318	8 ABM82457	Abm82457 Tumour-as
10	854	45.2	317	6 ADA83770	Ada83770 Human MAG
11	854	45.2	317	8 ADO59164	Ado59164 Human MAG
12	849	44.9	317	6 ABU56545	Abu56545 Lung canc
13	849	44.9	317	8 ADO43756	Ado43756 Human MAG
14	846.5	44.8	315	3 AAB08735	Aab08735 Amino aci
15	846.5	44.8	315	6 AAB08734	Abm82457 Tumour-as
16	846.5	44.8	315	6 ABU56684	Abu56684 Lung canc
17	846.5	44.8	315	6 ABU56484	Abu56484 Lung canc
18	846.5	44.8	315	6 ADA83772	Ada83772 Human MAG
19	846.5	44.8	315	6 ABU04413	Abu04413 Human exp
20	846.5	44.8	315	6 ABU04425	Abu04425 Human exp
21	846.5	44.8	315	6 ABU04421	Abu04421 Human exp
22	846.5	44.8	315	6 ABU04456	Abu04456 Human exp
23	846.5	44.8	315	6 ABU04454	Abu04454 Human exp
24	846.5	44.8	315	6 ABO25122	Abos2122 Human MAG
25	840.5	44.4	315	7 ADN39048	Adn39048 Cancer/an
			315	6 ABU04416	Abu04416 Human exp

26	827	43.7	317	2 AAY06998	Aay06998 MAGE-4 pr
27	811.5	42.9	316	6 ABU04419	Abu04419 Human exp
28	807	42.7	309	2 AAR70909	Aar70909 Human mel
29	807	42.7	309	2 AAW81548	Aaw81548 Tumour re
30	807	42.7	309	4 AAB31290	Aab31290 Amino aci
31	807	42.7	309	4 AAS06806	Aas06806 Human MAG
32	807	42.7	309	5 AAU84814	Aau84814 Human MAG
33	807	42.7	309	6 ABP74195	Abp74195 Human MAG
34	807	42.7	309	6 ABU08930	Abu08930 Human tum
35	807	42.7	309	7 ADC09573	Adc09573 MAGE-1 pr
36	807	42.7	309	7 ADG18028	Adg18028 MAGE-A1 p
37	807	42.7	309	7 ADM33110	Adm33110 Human MAG
38	807	42.7	309	8 ADI79402	Adi79402 Human MAG
39	807	42.7	309	8 ADR70544	Adr70544 Respirato
40	807	42.7	309	8 ADJ54143	Adj54143 Human MAG
41	807	42.7	309	8 ADM72812	Adm72812 Human MAG
42	807	42.7	309	8 ADQ36555	Adq36555 Human MAG
43	807	42.7	310	6 AAO19742	Aao19742 Wild-type
44	807	42.7	445	2 AAY06592	Aay06592 CLYTA-MAG
45	807	42.7	446	2 AAY06590	Aay06590 Lipoprote

ALIGNMENTS

RESULT 1
AAY71485
ID AAY71485 standard; protein; 369 AA.
XX AAY71485;
XX
DT 12-OCT-2000 (first entry)
XX
DE Human MAGE-A10 protein.
XX
KW MAGE-A10; human; Tumour Rejection Antigen; TRA; Human Leucocyte Antigen;
KW HLA; Major Histocompatibility Complex; MHC; cytolytic T-lymphocyte; CTL;
KW Immune response stimulator; prophylaxis; therapy; diagnosis; tumour;
KW cancer; TNF; tumour necrosis factor; cytostatic.
XX Homo sapiens.
OS
XX WO200032769-A2.
PN
XX
PD 08-JUN-2000.
XX
PF 26-NOV-1999; 99WO-IB002018.
XX
PR 27-NOV-1998; 98GB-00026143.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Huang L, Van Pel A, Brasseur F, De Plaen E, Boon T;
XX
DR WPI; 2000-412317/35.
XX
DR N-PSDB; AAD01311, AAD01312, AAD01313.
XX
PT Novel polypeptides expressed in tumor cells useful for treating cancers
PT have an ability to complex with a major histocompatibility complex
XX molecule and comprises a specific unbroken amino acid sequence.
XX
PS Claim 1; Fig 7; 80pp; English.
XX
CC The patent discloses MAGE-A10 and MAGE-A8 polypeptide, nonapeptide and
CC decapeptide sequences, that function as tumour rejection antigens (TRAAs).
CC These peptides are capable of forming a complex with major
CC histocompatibility complex (MHC) molecule types HLA-A2.1 (Human Leucocyte
CC Antigen), that are recognised by T-lymphocytes and elicit an immune
CC response from cytolytic T-lymphocytes (CTL). They function as an immune
CC response stimulator. Tumour rejection antigens are useful in prophylaxis,
CC therapy and diagnosis of tumours and are effective in controlling or
CC preventing tumour growth. The present sequence is the human MAGE-A10
CC protein, comprising nonapeptides and decapeptides, that serve as tumour

CC rejection antigens (TRA8). The novel TRAs encoded by MAG8-A10 is
 CC identified using melanoma cell line (LBI751-MEL), stimulated by
 CC autologous CTL clone (447A/5) to produce TNF (tumour necrosis factor).
 CC Expression of MAG8-A10 has been detected in a variety of tumours like
 CC melanomas, carcinomas of the head and neck, bladder and prostate,
 CC myelomas and lung cancer. The only normal tissue expressing MAG8-A10 is
 CC the testis
 XX
 SQ Sequence 369 AA;

Query Match 100.0%; Score 1891; DB 3; Length 369;
 Best Local Similarity 100.0%; Pred. No. 4.5e-156;
 Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRAPKRCRCMPEDLQSQSETQGLEGAQAPLAVEEDASSSTSTSSFPSPSSSSSS 60
 Db 1 MPRAPKRCRCMPEDLQSQSETQGLEGAQAPLAVEEDASSSTSTSSFPSPSSSSSS 60

Qy 61 SSCYPLIPSTPEEVSADDETPNPQSAQIACSSPSVVASLPDQSDGSSSQKEESPSTL 120
 Db 61 SSCYPLIPSTPEEVSADDETPNPQSAQIACSSPSVVASLPDQSDGSSSQKEESPSTL 120

Qy 121 QVLPDSESLPRSEIDEKVTDLVQFLFKYQMKPEPTKAEILSVIKNYEDHFFLLFSEAS 180
 Db 121 QVLPDSESLPRSEIDEKVTDLVQFLFKYQMKPEPTKAEILSVIKNYEDHFFLLFSEAS 180

Qy 181 ECVLLVFGIDVKEVDPTGHSFVLVTSGLTYDGMISDVQSMPTGILILISIFIRGYC 240
 Db 181 ECVLLVFGIDVKEVDPTGHSFVLVTSGLTYDGMISDVQSMPTGILILISIFIRGYC 240

Qy 241 TPEEVIWEALNMGLYDGMHEHLYGEPKLLTQDWQENLYEVQVPGSDPARVEFLWGP 300
 Db 241 TPEEVIWEALNMGLYDGMHEHLYGEPKLLTQDWQENLYEVQVPGSDPARVEFLWGP 300

Qy 301 RAHAERKMSLLKFLAKVNGSDPRSPFLWYEEALKDEEERAQDRIATTTDDTTAMASASS 360
 Db 301 RAHAERKMSLLKFLAKVNGSDPRSPFLWYEEALKDEEERAQDRIATTTDDTTAMASASS 360

Qy 361 ATGSFSYPE 369
 Db 361 ATGSFSYPE 369

RESULT 2
 AAB80297
 ID AAB80297 standard; protein; 369 AA.
 XX
 AC AAB80297;
 XX
 DT 24-APR-2001 (first entry)
 XX
 DE Human prostate cancer antigen #25.
 XX
 KW Immunosuppressive; neutropic; neuroprotective; antiviral; vulnary;
 KW anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant;
 KW immune disorder; cardiovascular disorder; neurological disease;
 KW infection; cancer; cytostatic; antiarthritic; antirheumatic;
 KW antiaethmatic; anticonvulsant; vasotropic; vulnary; human;
 KW secreted protein; prostate cancer antigen.
 XX
 OS Homo sapiens.
 XX
 PN WO200107476-A1.
 XX
 PD 01-FEB-2001.
 XX
 PF 20-JUL-2000; 2000WO-US019666.
 XX
 PR 21-JUL-1999; 99US-0144972P.
 PR 13-AUG-1999; 99US-0148681P.
 PR 17-AUG-1999; 99US-0149173P.
 PR 06-OCT-1999; 99US-0158004P.
 PR 05-APR-2000; 2000US-0194682P.

XX (HUMA-) HUMAN GENOME SCI INC.
 PA (ROSE)/ ROSEN C A.
 XX
 PI Rosen CA, Birse C;
 XX
 DR WPI; 2001-138554/14.
 DR N-PSDB; AAF72765.
 XX
 PT New nucleic acid molecule encoding human secreted prostate cancer
 PT antigens, useful for the diagnosis and treatment of disorders such as
 PT cancer, leukemia and autoimmune disease.
 XX
 PS Claim 11; Page 399-400; 433pp; English.

XX The present invention relates to human secreted prostate cancer antigen
 CC coding sequences (AAF72741-AAF72789) and proteins (AAB80273-AAB80321).
 CC The coding sequences and proteins of the present invention are useful for
 CC preventing, treating or ameliorating a medical condition; and for the
 CC diagnosis and treatment of diseases and disorders. Diseases and disorders
 CC that can be diagnosed and treated include (auto)immune diseases (e.g.
 CC graft versus host disease and rheumatoid arthritis), inflammatory and
 CC allergic disorders (e.g. asthma), hyperproliferative disorders (e.g.
 CC cancers and leukemias), cardiovascular disorders (e.g. heart attacks and
 CC arrhythmias), cerebrovascular disorders (e.g. stroke), arterial occlusive
 CC disorders (e.g. arteriosclerosis), angiogenesis related disorders (e.g.
 CC retinopathy and keloid scars), ocular disorders (e.g. glaucoma),
 CC neurological disorders (e.g. Alzheimer's, Parkinson's disease, epilepsy
 CC and Creutzfeld-Jakob disease) and infections caused by bacteria, fungi,
 CC viruses or parasites. They may also be useful for wound healing,
 CC epithelial cell proliferation, supporting cell culture, tissue
 CC regeneration, birth control and as a food additive or preservative
 XX
 SQ Sequence 369 AA;

Query Match 100.0%; Score 1891; DB 4; Length 369;
 Best Local Similarity 100.0%; Pred. No. 4.5e-156;
 Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRAPKRCRCMPEDLQSQSETQGLEGAQAPLAVEEDASSSTSTSSFPSPSSSSSS 60
 Db 1 MPRAPKRCRCMPEDLQSQSETQGLEGAQAPLAVEEDASSSTSTSSFPSPSSSSSS 60

Qy 61 SSCYPLIPSTPEEVSADDETPNPQSAQIACSSPSVVASLPDQSDGSSSQKEESPSTL 120
 Db 61 SSCYPLIPSTPEEVSADDETPNPQSAQIACSSPSVVASLPDQSDGSSSQKEESPSTL 120

Qy 121 QVLPDSESLPRSEIDEKVTDLVQFLFKYQMKPEPTKAEILSVIKNYEDHFFLLFSEAS 180
 Db 121 QVLPDSESLPRSEIDEKVTDLVQFLFKYQMKPEPTKAEILSVIKNYEDHFFLLFSEAS 180

Qy 181 ECVLLVFGIDVKEVDPTGHSFVLVTSGLTYDGMISDVQSMPTGILILISIFIRGYC 240
 Db 181 ECVLLVFGIDVKEVDPTGHSFVLVTSGLTYDGMISDVQSMPTGILILISIFIRGYC 240

Qy 241 TPEEVIWEALNMGLYDGMHEHLYGEPKLLTQDWQENLYEVQVPGSDPARVEFLWGP 300
 Db 241 TPEEVIWEALNMGLYDGMHEHLYGEPKLLTQDWQENLYEVQVPGSDPARVEFLWGP 300

Qy 301 RAHAERKMSLLKFLAKVNGSDPRSPFLWYEEALKDEEERAQDRIATTTDDTTAMASASS 360
 Db 301 RAHAERKMSLLKFLAKVNGSDPRSPFLWYEEALKDEEERAQDRIATTTDDTTAMASASS 360

Qy 361 ATGSFSYPE 369
 Db 361 ATGSFSYPE 369

RESULT 3
 ABR48215
 ID ABR48215 standard; protein; 369 AA.
 XX
 AC ABR48215;

XX DT 12-JUN-2003 (first entry)
XX DE Human bladder cancer associated protein sequence SEQ ID NO:149.
XX KW Human, bladder cancer; cytostatic; gene therapy; vaccine.
XX OS Homo sapiens.
XX FN WO2003003906-A2.
XX PD 16-JAN-2003.
XX PF 03-JUL-2002; 2002WO-US0211338.
XX PR 03-JUL-2001; 2001US-0302814P.
XX PR 03-AUG-2001; 2001US-0310099P.
XX PR 08-NOV-2001; 2001US-0343705P.
XX PR 13-NOV-2001; 2001US-0350666P.
XX PR 12-APR-2002; 2002US-0372246P.
XX PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX PI Mack DH, Aziz N;
XX WPI; 2003-201532/19.
XX N-PSDB; ACC51029.
XX PT Detecting a bladder cancer-associated transcript in a cell from a
XX patient, comprises contacting a biological sample from the patient with a
XX bladder cancer-associated polynucleotide or antibody.
XX PS Claim 10; Page 282; 307pp; English.
XX CC The present invention describes a method for detecting a bladder cancer-
XX associated transcript in a cell from a patient. The method comprises
XX contacting a biological sample from the patient with a polynucleotide
XX that selectively hybridizes to a sequence that is 80 % identical to a
XX table of sequences (see ACC50951 to ACC51059). ACC50951 to ACC51059
XX encode the human bladder cancer-associated proteins given in ABR48146 to
XX ABR48242). Bladder cancer-associated sequences from the present invention
XX have cytostatic activities, and can be used in antisense gene therapy and
XX in vaccine production. The method can be used for detecting a bladder
XX cancer-associated transcript in a cell from a patient. The method is
XX useful in diagnosing or treating bladder cancer and in screening for
XX compounds that modulate bladder cancer, such as hormones or antibodies.
XX The nucleic acid molecules from the present invention may be used in
XX various screening and diagnostic methods, and for gene therapy, vaccine
XX and/or antisense/inhibition applications
XX SQ Sequence 369 AA;
Query Match 100.0%; Score 1891; DB 6; Length 369;
Best Local Similarity 100.0%; Pred. No. 4.5e-156;
Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPRAKQRCMPEDLQSQETQLEGQAQPLAVEEDASSSTSTSSFPSPSSSSSS 60
DB 1 MPRAKQRCMPEDLQSQETQLEGQAQPLAVEEDASSSTSTSSFPSPSSSSSS 60
QY 61 SSCYPLIPSTPEVSADETPNPQSAQIACSSPSVVASLPDQSDGSSSQKEESPSTL 120
DB 61 SSCYPLIPSTPEVSADETPNPQSAQIACSSPSVVASLPDQSDGSSSQKEESPSTL 120
QY 121 QVLPDSLSRSEDEKVTDLQVLLPKYQKPEITKAEILSVIKNYDHPPLLFSEAS 180
DB 121 QVLPDSLSRSEDEKVTDLQVLLPKYQKPEITKAEILSVIKNYDHPPLLFSEAS 180
QY 181 ECLMLVFGIDVKEVDPTGHSPVLVTSGLTYDGMLSDVQSNPKTGILILISLIFIBGYC 240
DB 181 ECLMLVFGIDVKEVDPTGHSPVLVTSGLTYDGMLSDVQSNPKTGILILISLIFIBGYC 240
QY 241 TPBEVIWEALNMGLYDGMHEHLYGEBPRKLLTQDWQENLYEQVPGSDPARYEFLWGP 300

DB 241 TPBEVIWEALNMGLYDGMHEHLYGEBPRKLLTQDWQENLYEQVPGSDPARYEFLWGP 300
QY 301 RAHAERKMSLLKFLAKVNGSDPRSPFLMYERALKDEERAAQRIATTTDDTTAMASASS 360
DB 301 RAHAERKMSLLKFLAKVNGSDPRSPFLMYERALKDEERAAQRIATTTDDTTAMASASS 360
QY 361 ATGSPSYPE 369
DB 361 ATGSPSYPE 369
RESULT 4
ID ABUS6516 standard; protein; 369 AA.
XX AC ABUS6516;
XX DT 02-APR-2003 (first entry)
XX DE Lung cancer-associated polypeptide #109.
XX KW Lung cancer-associated polypeptide; cytostatic; emphysema;
XX antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;
XX small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
XX chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
XX interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
XX OS Unidentified.
XX WPI; 20020286443-A2.
XX PD 31-OCT-2002.
XX PF 18-APR-2002; 2002WO-US012476.
XX PR 18-APR-2001; 2001US-0284770P.
XX PR 10-MAY-2001; 2001US-0290492P.
XX PR 09-NOV-2001; 2001US-0339245P.
XX PR 13-NOV-2001; 2001US-0350666P.
XX PR 29-NOV-2001; 2001US-0334370P.
XX PR 12-APR-2002; 2002US-0372246P.
XX PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX PI Aziz N, Murray R;
XX WPI; 2003-093161/08.
XX N-PSDB; ABX76240.
XX PT Detecting a lung cancer-associated transcript in a cell from a patient
XX for treating lung cancer, by contacting a biological sample from the
XX patient with a polynucleotide that exhibits increased or decreased
XX expression in lung cancer.
XX PS Claim 27; Page 276-277; 453pp; English.
XX CC The invention relates to a method for detecting a lung cancer-associated
XX transcript in a cell from a patient, comprising contacting a biological
XX sample from the patient with a polynucleotide that selectively hybridizes
XX to a sequence that is at least 80 % identical to a gene that exhibits
XX increased or decreased expression in lung cancer samples. Lung cancer-
XX associated polynucleotides and polypeptides are used for identifying a
XX compound that modulates a lung cancer-associated polypeptide, for
XX inhibiting proliferation of a lung cancer-associated cell to treat lung
XX cancer in a patient and for treating a mammal having lung cancer by
XX administering a modulatory compound identified. The methods are useful
XX for treating lung cancer, such as small cell lung cancer, non-small cell
XX lung cancer or other benign or precancerous lesions, e.g. atelectasis,
XX emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,
XX hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and
XX bronchiectasis. The genes, polynucleotides and polypeptides are useful
XX for diagnostic purposes and as targets for screening for therapeutic

```
CC compounds that modulate lung cancer, such as antibodies. Sequences
CC ABU56408-ABU56745 represent lung cancer-associated polypeptides of the
CC invention
XX
XX
SQ Sequence 369 AA;
  Query Match      100.0%; Score 1891; DB 6; Length 369;
  Best Local Similarity 100.0%; Pred. No. 4.5e-156;
  Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MPRAPKRCRCMPEDLQSQSETQGLGGAQAPLAVEEDASSSTSTSSPSPSPSSSSSS 60
Db 1 MPRAPKRCRCMPEDLQSQSETQGLGGAQAPLAVEEDASSSTSTSSPSPSPSSSSSS 60
Qy 61 SSCYPLIPSTPEEVSADDETPNPQSAQIACSSPSVVASLPDQSDGSSSQKEESPSTL 120
Db 61 SSCYPLIPSTPEEVSADDETPNPQSAQIACSSPSVVASLPDQSDGSSSQKEESPSTL 120
Qy 121 QVLPDSSESLPRSEIDKVTDLVQFLFKYQKKEPITKAEILLESVKNYEDHFFLLFSEAS 180
Db 121 QVLPDSSESLPRSEIDKVTDLVQFLFKYQKKEPITKAEILLESVKNYEDHFFLLFSEAS 180
Qy 181 ECMLLVFGIDVKEVDPTGHSFVLVTSGLTYDGMLSDVQSMPTGILILLSIIFIEGYC 240
Db 181 ECMLLVFGIDVKEVDPTGHSFVLVTSGLTYDGMLSDVQSMPTGILILLSIIFIEGYC 240
Qy 241 TPEEVIWEALNMGLYDGMHEHLYGPRKLLTQDWQENYLEYRQVPGSDPARYEFWLGP 300
Db 241 TPEEVIWEALNMGLYDGMHEHLYGPRKLLTQDWQENYLEYRQVPGSDPARYEFWLGP 300
Qy 301 RAHAIRKMSLLKFLAKVNGSDPRSPFLWYEEALKDDEERAQDRIATDDTTAMASASS 360
Db 301 RAHAIRKMSLLKFLAKVNGSDPRSPFLWYEEALKDDEERAQDRIATDDTTAMASASS 360
Qy 361 ATGFSFSYPE 369
Db 361 ATGFSFSYPE 369
RESULT 5
ID ABO58424 standard; protein; 383 AA.
AC ABO58424;
XX
XX 29-JUL-2004 (first entry)
XX Human genome derived single exon protein #4658.
DE Human; gene expression; single exon probe; microarray;
KW alternative splicing event; genomic alteration.
XX Homo sapiens.
XX US2003194704-A1.
XX 16-OCT-2003.
XX
XX 03-APR-2002; 2002US-00029386.
XX
XX 03-APR-2002; 2002US-00029386.
XX (PENN/) PENN S G.
XX (RANK/) RANK D R.
XX (HANZ/) HANZEL D K.
XX Penn SG, Rank DR, Hanzel DK;
XX WPI; 2004-119264/12.
XX
XX New human genome-derived single exon nucleic acid probes useful for human
XX gene expression analysis, for identifying or characterizing alternative
XX splicing events, for assessing genomic alterations or as tools for
```

```
PT surveying tissues.
XX Claim 45; SEQ ID NO 32058; 80pp; English.
XX
CC The invention relates to a nucleic acid probe for measuring human gene
CC expression, comprising any of the 27,400 fully defined nucleotide
CC sequences in the specification, or their complements or fragments, and
CC encoding at least 8 amino acids of any of the 6888 amino acid sequences
CC fully defined in the specification. The probe is a single exon probe that
CC hybridises under high stringency conditions to a nucleic acid molecule
CC expressed in human cells or tissues. Also included are a spatially-
CC addressable set of single exon nucleic acid probes for measuring human
CC gene expression (comprising a plurality of single exon nucleic acid
CC probes cited above, where each of the plurality of probes is separately
CC and addressably isolatable or amplifiable from the plurality), a single
CC exon microarray for measuring human gene expression, a method of
CC measuring human gene expression, a vector comprising the single exon
CC probe cited above, an ORF-encoded peptide comprising at least 8
CC contiguous amino acids of any of the above-mentioned amino acid
CC sequences (optionally with conservative amino acid substitutions), an
CC isolated antibody that binds specifically to a peptide cited above,
CC methods of selling and/or licensing single exon probes or microarrays to
CC a customer desiring to measure gene expression, a method of providing
CC human gene expression data by subscription, and a computer-readable
CC storage medium which contains a database having a plurality of records
CC (each record including data on the expression of a single exon probe
CC cited above). The probe, methods and apparatus are useful in gene
CC expression analysis. The probes may be used as tools for surveying
CC tissues to detect the presence of expressed messages that contain their
CC specific exon, or in constructing genome-derived single exon microarrays.
CC In addition, the probes are used in identifying and characterising
CC alternative splicing events, in detecting and characterising gross
CC alterations in the genomic locus that includes their exon, in assessing
CC smaller genomic alterations, in priming the synthesis of nucleic acids,
CC or in expressing the ORF-encoded peptide. The present sequence is a human
CC single exon probe protein of the invention. Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20030194704
XX
SQ Sequence 383 AA;
  Query Match      97.9%; Score 1852; DB 8; Length 383;
  Best Local Similarity 100.0%; Pred. No. 1.2e-152;
  Matches 362; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MPRAPKRCRCMPEDLQSQSETQGLGGAQAPLAVEEDASSSTSTSSPSPSPSSSSSS 60
Db 22 MPRAPKRCRCMPEDLQSQSETQGLGGAQAPLAVEEDASSSTSTSSPSPSPSSSSSS 81
Qy 61 SSCYPLIPSTPEEVSADDETPNPQSAQIACSSPSVVASLPDQSDGSSSQKEESPSTL 120
Db 82 SSCYPLIPSTPEEVSADDETPNPQSAQIACSSPSVVASLPDQSDGSSSQKEESPSTL 141
Qy 121 QVLPDSSESLPRSEIDKVTDLVQFLFKYQKKEPITKAEILLESVKNYEDHFFLLFSEAS 180
Db 142 QVLPDSSESLPRSEIDKVTDLVQFLFKYQKKEPITKAEILLESVKNYEDHFFLLFSEAS 201
Qy 181 ECMLLVFGIDVKEVDPTGHSFVLVTSGLTYDGMLSDVQSMPTGILILLSIIFIEGYC 240
Db 202 ECMLLVFGIDVKEVDPTGHSFVLVTSGLTYDGMLSDVQSMPTGILILLSIIFIEGYC 261
Qy 241 TPEEVIWEALNMGLYDGMHEHLYGPRKLLTQDWQENYLEYRQVPGSDPARYEFWLGP 300
Db 262 TPEEVIWEALNMGLYDGMHEHLYGPRKLLTQDWQENYLEYRQVPGSDPARYEFWLGP 321
Qy 301 RAHAIRKMSLLKFLAKVNGSDPRSPFLWYEEALKDDEERAQDRIATDDTTAMASASS 360
Db 322 RAHAIRKMSLLKFLAKVNGSDPRSPFLWYEEALKDDEERAQDRIATDDTTAMASASS 381
Qy 361 AT 362
Db 382 AT 383
```

RESULT 6
 ID ADR09600 standard; protein; 394 AA.
 XX AC ADR09600;
 XX DT 04-NOV-2004 (first entry)
 XX DE Human protein useful for treating neurological disease Seq 3106.
 XX KW human; oligo-capping method; diagnostic marker; gene therapy;
 XX KW osteoporosis; neurological disease; Alzheimer's disease;
 KW Parkinson's disease; dementia; short memory; cancer;
 KW sense or motor function; emotional reaction; fear response; panic;
 KW osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;
 KW tranquiliser.
 XX OS Homo sapiens.
 XX PN EPI447413-A2.
 XX PD 18-AUG-2004.
 XX PF 12-FEB-2004; 2004EP-00003145.
 XX PR 14-FEB-2003; 2003JP-00102207.
 XX PR 09-MAY-2003; 2003JP-00131452.
 XX (REAS-) RES ASSOC BIOTECHNOLOGY.
 XX PA Isogai T, Yamamoto J, Nishikawa T, Isono Y, Sugiyama T, Otsuki T;
 PI Wakamatsu A, Ishii S, Nagai K, Irie R;
 XX WPI; 2004-583265/57.
 DR N-PSDB; ADR0764.
 XX New 1995 cDNA, useful for treating osteoporosis, neurological diseases,
 PT Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
 PS Claim 1; SEQ ID NO 3106; 2686pp; English.
 CC This invention relates to novel, isolated full length human cDNA
 CC molecules and the encoded proteins thereof. Specifically, it refers to
 CC cDNA clones obtained by an oligo-capping method, where none of these
 CC clones are identical to any known human mRNAs. The present invention
 CC describes an immunassay to identify agonists and antagonists, as well as
 CC antibodies, antisense molecules and siRNAs that can all be used to bind
 CC to and modulate expression of the cDNA molecules. As such, these
 CC molecules are useful for diagnostic markers or therapeutic targets for
 CC the various diseases or morbid states. In particular, they are useful in
 CC gene therapy for treating osteoporosis, neurological disease, Alzheimer's
 CC disease, Parkinson's disease, dementia, short memory and various cancers,
 CC as well as for maintaining equilibrium of sense or motor function, and
 CC for treating emotional reaction, fear response and panic. Accordingly,
 CC they exhibit osteopathic, neuroprotective, nootropic, antiparkinsonian,
 CC cytostatic and tranquiliser activities. This polypeptide is a protein
 CC encoded by a full length human cDNA sequence of the invention. NOTE: This
 CC sequence is not given in the sequence listing of the specification but
 CC can be obtained on CD-ROM from the European Patent Office, Vienna Sub-
 CC office.
 XX Sequence 394 AA;
 SQ
 Query Match 48.2%; Score 911; DB 8; Length 394;
 Best Local Similarity 54.0%; Pred. No. 1.6e-70;
 Matches 183; Conservative 53; Mismatches 81; Indels 22; Gaps 2;
 QY 1 MPRAKQRCWPEEDLQSQSTQGLEGAQAPLAVEDASSSTSTSSFPSSSSSSSS 60
 DB 76 MPEQRQHCPEGLQAEEDLGLVGAQALQAEQEAAPFSST----- 119

61 SSCYPLIPSTPERVSADDETPNPQSAQIACSPSVVASLPDQSDGSSSQKESPSSTL 120
 120 -----LNVGTLLELPA-AESPSPQSPQERSFPTAMDAIFGSLSDGSGSQKESGSPST 173
 121 QVLPDSESLPRSEIDKVTDLVQFLFKYQKMEPITKAEILESVIKYVEDHDFPLSEAS 180
 174 PDLIDPESFSQDILHDKIIDLVHLLLRKYRKGILITKAEMLGSVIKNYEDYFPEIFREAS 233
 181 ECLLVFGIDVKEVDPTGHSFVLVTSLGLTYDQMLSDVQSMPTKGIILILISIIFFIEGYC 240
 234 VCQLLFGIDVKEVDPTGHSFVLVTSLGLTYDQMLSDVQSMPTKGIILILISIIFFIEGYC 293
 241 TPBEVWEALNMGLYDGMHEHLYIGBPRKLLTQDWOENYLEYRQVPGSDPARYEFELWGP 300
 294 IPBEVWMEVLISMGVYAGREHFLFGBPKRLLTQWVQEKYLVYRQVGTDPACVEFLWGP 353
 301 RAHAKRKMSLLFLAKVNGSDPRSPPLWYEEALKDDEE 339
 354 RAHAKTSKMKVLYBIANANRDRPTSPSLYEDALREGR 392

RESULT 7
 AAB08736
 ID AAB08736 standard; protein; 429 AA.
 XX AC AAB08736;
 XX DT 02-JAN-2001 (first entry)
 XX DE Amino acid sequence of a human MAGE-A11 polypeptide.
 XX KW MAGE-A5; MAGE-A8; MAGE-A9; MAGE-A11; tumour rejection antigen;
 KW human leukocyte antigen; HLA; T cell response; region q28; X chromosome;
 KW cancer.
 XX OS Homo sapiens.
 XX PN WO200052163-A1.
 XX PD 08-SEP-2000.
 XX PF 01-MAR-2000; 2000WO-US005346.
 XX PR 02-MAR-1999; 99US-00260978.
 XX (LUDM-) LUDWIG INST CANCER RES.
 XX PI Serrano A, Lethe B, Lurquin C, De Plaen E, Rimoldi D;
 PI Boon-Falleur T;
 XX WPI; 2000-579285/54.
 DR N-PSDB; AAA64635.
 XX Complementary polynucleotide of MAGE family, useful in the diagnosis of
 PT cancer in a patient.
 XX Example 4; Page 66-68; 72pp; English.
 CC The present sequence represents a human MAGE-A11 polypeptide. The
 CC specification also describes MAGE-A5, MAGE-A8, MAGE-A9, and MAGE-A11
 CC polypeptides. The MAGE genes encode tumour rejection antigens which
 CC complex to human leukocyte antigens (HLAs), and provoke response by
 CC autologous, cytolytic T cells. The genes are located in region q28 of the
 CC X chromosome. The MAGE polynucleotides are useful for diagnosis of cancer
 CC in a patient
 XX Sequence 429 AA;
 SQ
 Query Match 48.2%; Score 911; DB 3; Length 429;
 Best Local Similarity 54.0%; Pred. No. 1.8e-70;
 Matches 183; Conservative 53; Mismatches 81; Indels 22; Gaps 2;
 QY 1 MPRAKQRCWPEEDLQSQSTQGLEGAQAPLAVEDASSSTSTSSFPSSSSSSSS 60

```

Db 111 MPLSORSQCHCKPEEGLOAQEDLGLVGAALQAEEQEAFFSST----- 154
Qy 61 SSCYPLIPSTPEEVSADDETNPQSAQIACSSPSVVASLPDQSDGSSQKESPESTL 120
Db 155 -----LNVGTLEELPA-AESPPSPQSEFSPTAMDAIFGSLSDGSGSQEKGFPST 208
Qy 121 QVLPDSLSLPRSEIDEKVTDLVQFLFKYQMKERITKAEIILESIVKNYEDHPFLLPSEAS 180
Db 209 PDLIDPSFSQDIILDKIIDLHLLLRKYRKGLITKAEMLGSKVKNYEDIFPEIFREAS 268
Qy 181 ECLMLVFGIDVKEVDPTGSHSVLTSLGLTYDGMCLSDVQSMPTKGLILILSIIFIBGYC 240
Db 269 VCMQLLFGIDVKEVDPTGSHSVLTSLNLSYDQCNEQSMPSKGLLIIVLGVIFMEGNC 328
Qy 241 TPEEVIWEALNMGLYDGMHLLIYGEPRKLLTQDWQVQNYLEYRQVPGSDPARVEFLWGP 300
Db 329 IPEEVMVEVLGIMGVYAGREHFLFGEPRKLLTONWVQEKYLVYRQVPGTDPACYEFLWGP 388
Qy 301 RAHAERKMSLLKFLAKVNGSDPRSPFLWYEEALKDEE 339
Db 389 RAHAETSKMKVLEXYANANGRDPTSYPELYEDALREGE 427

```

RESULT 8

AA08734
ID AA08734 standard; protein; 318 AA.

AC AA08734;

DT 02-JAN-2001 (first entry)

DE Amino acid sequence of a human MAGE-A8 polypeptide.

XX MAGE-A5; MAGE-A8; MAGE-A9; MAGE-A11; tumour rejection antigen;
KW human leukocyte antigen; HLA; T cell response; region q28; X chromosome;
KW cancer.

XX Homo sapiens.

XX WO200052163-A1.

XX 08-SEP-2000.

XX 01-MAR-2000; 2000WO-US005346.

XX 02-MAR-1999; 99US-00260978.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Serrano A, Lethe B, Lurquin C, De Plaen E, Rimoldi D;
PI Boon-Falleur T;

XX WPI; 2000-579285/54.

XX N-PSDB; AAA64633.

XX Complementary polynucleotide of MAGE family, useful in the diagnosis of
PT cancer in a patient.

XX Example 4; Page 62-64; 72pp; English.

XX The present sequence represents a human MAGE-A8 polypeptide. The
CC specification also describes MAGE-A5, MAGE-A8, MAGE-A9, and MAGE-A11
CC polypeptides. The MAGE genes encode tumour rejection antigens which
CC complex to human leukocyte antigens (HLAs), and provoke response by
CC autologous, cytolytic T cells. The genes are located in region q28 of the
CC X chromosome. The MAGE polynucleotides are useful for diagnosis of cancer
CC in a patient

XX Sequence 318 AA;

Query Match 48.1%; Score 910; DB 3; Length 318;
Best Local Similarity 56.5%; Pred. No. 1.4e-70;

```

Matches 188; Conservative 45; Mismatches 78; Indels 22; Gaps 2;
Qy 6 KRRCMPEDLDQSETQGLEGAQAPLAVEDASSSTSTSSPSSPSSSSSSSSSCYP 65
Db 6 KSQRYKAEGLQAQGEAPGLMDVQIPTAEERKAASSST----- 44
Qy 66 LIPSTPEVSADDETNPQSAQIACSSPSVVASLPDQSDGSSQKESPSSTLQVLPD 125
Db 45 LINGTLEEV-DSGSPSPQSPGASSSLVTUSTLWSQSDGSSNEEGPSTSPPAH 103
Qy 126 SESLPRSEIDEKVTDLVQFLFKYQMKERITKAEIILESIVKNYEDHPFLLPSEACMLL 185
Db 104 LESLFREALDEKVAELVRFLRKVQKEPVTKAEMLSEVKNYKNHPDFIFSKASECMQV 163
Qy 186 VFGIDVKEVDPTGSHSVLTSLGLTYDGMCLSDVQSMPTKGLILILSIIFIBGYCTPEEV 245
Db 164 IFGIDVKEVDPAHSHVILVTCGLSYDGLGDDQSTPKTGLLIIVLGMILMEGSRAPAEA 223
Qy 246 IWEALNMGLYDGMHLLIYGEPRKLLTQDWQVQNYLEYRQVPGSDPARVEFLWGPRAHAE 305
Db 224 IWEALSVNGLYDGRHSVYWKRLKLLTQEWQVQNYLEYRQVPGSDPVRYEFLWGPRAAE 283
Qy 306 IRKMSLLKFLAKVNGSDPRSPFLWYEEALKDEE 338
Db 284 TSYVKVLEHVVRVNRVIRISYPSLHREALGEEK 316

```

RESULT 9

ABM82457

ID ABM82457 standard; protein; 318 AA.

AC ABM82457;

DT 18-NOV-2004 (first entry)

DE Tumour-associated antigenic target (TAT) polypeptide PRO81395, SEQ:6309.

XX Tumour-associated antigenic target; TAT; human; overexpression; cancer;
KW tumour; diagnosis; cell proliferative disorder; breast cancer;
KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;
KW central nervous system cancer; bladder cancer; pancreatic cancer;
KW cervical cancer; melanoma; leukaemia; hybridisation probe;
KW chromosome identification; chromosome mapping; gene mapping;
KW gene therapy; cytostatic.

XX Homo sapiens.

XX WO2004030615-A2.

XX 15-APR-2004.

XX 29-SEP-2003; 2003WO-US028547.

XX 02-OCT-2002; 2002US-0414971P.

XX (GETH) GENENTECH INC.

XX Wu TD, Zhang Z, Zhou Y;

XX WPI; 2004-347921/32.

XX N-PSDB; ACN41095.

XX New tumor-associated antigenic target polypeptides and nucleic acids,
PT useful in preparing a medicament for treating or detecting a
PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or
PT prostate cancer or tumor.

XX Claim 12; SEQ ID NO 6309; 7273pp; English.

XX The invention relates to human tumour-associated antigenic target (TAT)
CC polypeptides, and their related nucleic acids. The TAT polypeptides are
CC overexpressed in cancer tissues compared to normal tissues, and may thus
CC serve as effective targets for the diagnosis and treatment of cancer in


```

XX DE Human MAGE-A4 related protein SeqID 1.
XX DE human; anticancer; melanoma antigen; MAGE-A4; cytostatic; hepatic cancer;
KW gankyrin; Gann ankyrin repeat protein; PSM10; P28; oncogene;
XX tumorigenesis.
XX OS Homo sapiens.
XX JP2004123752-A.
XX PD 22-APR-2004.
XX 02-OCT-2003; 2003JP-00344979.
XX 02-OCT-2002; 2002US-0415104P.
XX (FUJI/) FUJITA J.
XX WPI; 2004-323475/30.
XX N-PSDB; ADO59165.
XX Novel cytostatic agent for cancers expressing gankyrin, comprising
XX melanoma antigen (MAGE)-A4 related protein and having binding property
XX with gankyrin, useful as preventive or therapeutic agent of cancer.
XX Claim 1; SEQ ID NO 1; 22pp; Japanese.
XX This invention relates to a novel anticancer agent that comprises the
XX melanoma antigen MAGE-A4 related protein. Specifically, it refers to a
XX MAGE-A4 containing cytostatic agent useful for treating hepatic cancers
XX that highly express gankyrin, where gankyrin is a Gann ankyrin repeat
XX protein also known as PSM10 or the P28 oncogene. The present invention
XX describes using MAGE-A4 as a preventative or therapeutic agent to
XX suppress gankyrin activity and hence tumorigenesis. This polypeptide
XX sequence is the human MAGE-A4 related protein of the invention.
XX SQ Sequence 317 AA;

Query Match 45.2%; Score 854; DB 8; Length 317;
Best Local Similarity 51.9%; Pred. No. 1.1e-65;
Matches 176; Conservative 51; Mismatches 88; Indels 24; Gaps 3;

QY 1 MPRAPKRCRCMPREDLQSQSTQGLEGAQAAPLAVEEDASSSTSTSSFPSPSSSSSS 60
DB 1 MSSSQKSHCKPEEGVEAQEALGLVGAQAPTTEEQEAIVSSSS----- 44

QY 61 SSCYPLIPSTPEVSADDETPNPQQAQACSSPSVVASLPLDQSDGSSSQKEESPSTL 120
DB 45 ----PLVPGTLEEVPA-AESAGPPQSPQAGASALPTTISFTCWRQPNEGSSSQKEEGFST- 98

QY 121 QVLPDSLSLPRSEIDKQVTLVQFLPKYQKKEPTKAEILSVTKYEDHFPPLPSEAS 180
DB 99 --SPDAESLFRALSNKVDLHFLKRYAKELVTKAEMLERVKNKRCFPVIFGKAS 156

QY 181 ECLMLVFGIDVKEVDPGTGHSPLVTLGLTYDGMISDVQSMPTKGLILILIFIRGYC 240
DB 157 ESLKMIFGIDVKEVDPSTNTYTLVTCGLSDYDGLGNQIPFKTGLLILVLTGTTAMGDS 216

QY 241 TPEEVIWEALMMGLYDGMELIYGEPRKLLTQDWQENLYEYRQVFGSDPARYEFLWGP 300
DB 217 ASBEEIWEELGVMGVYDGREHTVYGEPRKLLTQDWQENLYEYRQVFGSDPARYEFLWGP 276

QY 301 RAHAIRKMSLLKFLAKNGSDRPSFPLWYEALKDEEE 339
DB 277 RALAETSIVKLEHVVRNARVRIAYPSLREALLLEEE 315

RESULT 12
ABU56545
ID ABU56545 standard; protein; 317 AA.
XX AC ABU56545;

```

```

XX 02-APR-2003 (first entry)
XX Lung cancer-associated polypeptide #138.
XX Lung cancer-associated polypeptide; cytostatic; emphysema;
KW antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;
KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
XX Unidentified.
XX OS WO200286443-A2.
XX 31-OCT-2002.
XX 18-APR-2002; 2002WO-US012476.
XX 18-APR-2001; 2001US-0284770P.
XX 10-MAY-2001; 2001US-0290492P.
XX 09-NOV-2001; 2001US-0339245P.
XX 13-NOV-2001; 2001US-0350666P.
XX 29-NOV-2001; 2001US-0334370P.
XX 12-APR-2002; 2002US-0372246P.
XX (EOSB-) EOS BIOTECHNOLOGY INC.
XX Aziz N, Murray R;
XX WPI; 2003-0933161/08.
XX N-PSDB; ABX76273.
XX Detecting a lung cancer-associated transcript in a cell from a patient
XX for treating lung cancer, by contacting a biological sample from the
XX patient with a polynucleotide that exhibits increased or decreased
XX expression in lung cancer.
XX Claim 27; Page 294; 453pp; English.
XX The invention relates to a method for detecting a lung cancer-associated
XX transcript in a cell from a patient, comprising contacting a biological
XX sample from the patient with a polynucleotide that selectively hybridises
XX to a sequence that is at least 80 % identical to a gene that exhibits
XX increased or decreased expression in lung cancer samples. Lung cancer-
XX associated polynucleotides and polypeptides are used for identifying a
XX compound that modulates a lung cancer-associated polypeptide, for
XX inhibiting proliferation of a lung cancer-associated cell to treat lung
XX cancer in a patient and for treating a mammal having lung cancer by
XX administering a modulatory compound identified. The methods are useful
XX for treating lung cancer, such as small cell lung cancer, non-small cell
XX lung cancer or other benign or precancerous lesions, e.g. atelectasis,
XX emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,
XX hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and
XX bronchiectasis. The genes, polynucleotides and polypeptides are useful
XX for diagnostic purposes and as targets for screening for therapeutic
XX compounds that modulate lung cancer, such as antibodies. Sequences
XX ABU56408-ABU56745 represent lung cancer-associated polypeptides of the
XX invention
XX SQ Sequence 317 AA;

Query Match 44.9%; Score 849; DB 6; Length 317;
Best Local Similarity 51.8%; Pred. No. 3e-65;
Matches 175; Conservative 51; Mismatches 89; Indels 24; Gaps 3;

QY 1 MPRAPKRCRCMPREDLQSQSTQGLEGAQAAPLAVEEDASSSTSTSSFPSPSSSSSS 60
DB 1 MSSEQKSHCKPEEGVEAQEALGLVGAQAPTTEEQEAIVSSSS----- 44

QY 61 SSCYPLIPSTPEVSADDETPNPQQAQACSSPSVVASLPLDQSDGSSSQKEESPSTL 120
DB 45 ----PLVPGTLEEVPA-AESAGPPQSPQAGASALPTTISFTCWRQPNEGSSSQKEEGFST- 98

```


QY 121 QVLPDSESLPRSEIDEKVTDLVQFLFKYQMKPEITKAEILSVIKNYEDHFFLLPSEAS 180
 DB 99 --SPDAESLPREALSNKVDLAHLAKRYAKELVTKAEMLERVIKYNKRCFFVIFGKAS 156
 QY 181 ECLMLVFGIDVKEVDPTGHSFVLVTSGLTYDGMCLSDVQSMPTGILILISLIFIEGYC 240
 DB 157 ESKMIFGIDVKEVDPTGHSFVLVTSGLTYDGMCLSDVQSMPTGILILISLIFIEGYC 216
 QY 241 TPEEVIWEALNMGLYDGMCLSDVQSMPTGILILISLIFIEGYC 300
 DB 217 ASEEEIWEELGVNGVDGHSFVLVTSGLTYDGMCLSDVQSMPTGILILISLIFIEGYC 276
 QY 301 RAHAIRKMSLLKFLAKVNGSDPRSPPLWYEEALKDEEE 339
 DB 277 RALAETSYVKLEHVVRNARVRIATPSLREAALEEE 315
 RESULT 13
 ID ADO43756 standard; protein; 317 AA.
 XX ADO43756;
 AC ADO43756;
 DT 15-JUL-2004 (first entry)
 DE Human MAGE-A4 polypeptide.
 KW Human; MAGE-A4; human leukocyte antigen; HLA class I-binding peptide;
 KW HLA-B37; CD8+ cytotoxic T lymphocyte; cancer; melanoma; myeloma;
 KW leukaemia; cytotatic.
 OS Homo sapiens.
 XX US2004033541-A1.
 XX 19-FEB-2004.
 XX 13-AUG-2002; 2002US-00218095.
 XX 13-AUG-2002; 2002US-00218095.
 XX (ZHAN/) ZHANG Y.
 XX (STRO/) STROOBANT V.
 XX (RUSS/) RUSSO V.
 XX (BOON/) BOON-FALLEUR T.
 XX (BRUG/) BRUGGEN P V D.
 XX Zhang Y, Stroobant V, Russo V, Boon-Falleur T, Bruggen PVD;
 XX WPI; 2004-447526/42.
 XX N-PSDB; ADO43755.
 XX Novel MAGE-A4 human leukocyte antigen class I-binding peptide, useful for
 XX treating a subject having a disorder with expression of MAGE-A4.
 XX Claim 4; SEQ ID NO 2; 40pp; English.
 XX The present invention relates to MAGE-A4 human leukocyte antigen (HLA)
 XX class I-binding peptides, and their use. The antigenic peptides derived
 XX from MAGE-A4, when presented by HLA-B37, induce the activation and
 XX proliferation of CD8+ cytotoxic T lymphocytes. Also disclosed are the
 XX polypeptide and polynucleotide sequences for human MAGE-A4. The peptides
 XX of the invention are useful for treating a subject having a disorder with
 XX aberrant expression of MAGE-A4. Such disorders particularly include
 XX cancer, e.g. melanoma, myeloma or leukaemias. The present sequence
 XX represents human MAGE-A4 polypeptide.
 XX Sequence 317 AA;

Query Match 44.9%; Score 849; DB 8; Length 317;
 Best Local Similarity 51.6%; Pred. No. 3e-65;
 Matches 175; Conservative 51; Mismatches 89; Indels 24; Gaps 3;

QY 1 MPRAPKQRKMPBEDLQSQSETOGLEGAQAPLAVEEDASSSTSTSSSPSPSSSSSS 60
 DB 1 MSSEQKSOHCKPBEQVGAQEEALGLVGAQAPTEEQEAIVSSSS----- 44
 QY 61 SSCYPLIPSTPERSVADDETFNPQSAQIACSSPSVVASLPLDQSDGSSSQKEESPSTL 120
 DB 45 ---PLVPFGTLEEVPA-ABSAGPPQSPQASALPTTISFTCMRQPNBSSSQBEEGPST- 98
 QY 121 QVLPDSESLPRSEIDEKVTDLVQFLFKYQMKPEITKAEILSVIKNYEDHFFLLPSEAS 180
 DB 99 --SPDAESLPREALSNKVDLAHLAKRYAKELVTKAEMLERVIKYNKRCFFVIFGKAS 156
 QY 181 ECLMLVFGIDVKEVDPTGHSFVLVTSGLTYDGMCLSDVQSMPTGILILISLIFIEGYC 240
 DB 157 ESKMIFGIDVKEVDPTGHSFVLVTSGLTYDGMCLSDVQSMPTGILILISLIFIEGYC 216
 QY 241 TPEEVIWEALNMGLYDGMCLSDVQSMPTGILILISLIFIEGYC 300
 DB 217 ASEEEIWEELGVNGVDGHSFVLVTSGLTYDGMCLSDVQSMPTGILILISLIFIEGYC 276
 QY 301 RAHAIRKMSLLKFLAKVNGSDPRSPPLWYEEALKDEEE 339
 DB 277 RALAETSYVKLEHVVRNARVRIATPSLREAALEEE 315
 RESULT 14
 ID AAB08735 standard; protein; 315 AA.
 AC AAB08735;
 DT 02-JAN-2001 (first entry)
 DE Amino acid sequence of a human MAGE-A9 polypeptide.
 KW MAGE-A5; MAGE-A8; MAGE-A9; MAGE-A11; tumour rejection antigen;
 KW human leukocyte antigen; HLA; T cell response; region q28; X chromosome;
 KW cancer.
 OS Homo sapiens.
 XX WO200052163-A1.
 XX 08-SEP-2000.
 XX 01-MAR-2000; 2000WO-US005346.
 XX 02-MAR-1999; 99US-00260978.
 XX (LUDW-) LUDWIG INST CANCER RES.
 XX Serrano A, Lethe B, Lurquin C, De Plaen E, Rimoldi D;
 XX Boon-Falleur T;
 XX WPI; 2000-579285/54.
 XX N-PSDB; AAA64634.
 XX Complementary polynucleotide of MAGE family, useful in the diagnosis of
 XX cancer in a patient.
 XX Example 4; Page 64-66; 72pp; English.
 XX The present sequence represents a human MAGE-A9 polypeptide. The
 XX specification also describes MAGE-A5, MAGE-A8, MAGE-A9, and MAGE-A11
 XX polypeptides. The MAGE genes encode tumour rejection antigens which
 XX complex to human leukocyte antigens (HLA), and provoke response by
 XX autologous, cytolytic T cells. The genes are located in region q28 of the
 XX X chromosome. The MAGE polynucleotides are useful for diagnosis of cancer
 XX in a patient
 XX Sequence 315 AA;

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 15, 2005, 15:32:22 ; Search time 51.7381 Seconds
(without alignments)
686.225 Million cell updates/sec

Title: US-09-856-812b-1
Perfect score: 1891
Sequence: 1 MPRAPKRCMPEDLQSQS.....DTTAMASASSSATGFSFSYPE 369

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR.79:.*
1: Pirl1.*
2: Pirl2.*
3: Pirl3.*
4: Pirl4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1891	100.0	369	2 I38659	melanoma antigen M
2	911	48.2	319	2 I38660	melanoma antigen M
3	849	44.9	317	2 I38661	melanoma antigen M
4	846.5	44.8	315	2 I38668	melanoma antigen M
5	800.5	42.3	314	2 I68899	melanoma antigen M
6	798.5	42.2	314	2 J23360	melanoma antigen M
7	783.5	41.4	314	2 J23361	melanoma antigen M
8	777.5	41.1	314	2 I54519	melanoma antigen M
9	766	40.5	280	2 J23358	melanoma antigen M
10	731	38.7	347	2 I38008	melanoma antigen M
11	639	33.8	234	2 I38667	melanoma antigen M
12	440.5	23.3	476	2 T43464	hypothetical prote
13	372	19.7	325	2 JN0148	necdin, brain - mo
14	222.5	11.8	133	2 I38663	melanoma antigen M
15	126.5	6.7	948	2 T11678	hypothetical prote
16	124	6.6	406	2 S38170	SRP40 protein - ye
17	122	6.5	1104	2 S59310	probable membrane
18	121	6.4	1791	2 T02345	hypothetical prote
19	120.5	6.4	1367	1 S48478	glucan 1,4-alpha-g
20	119.5	6.3	645	2 T49702	related to DOS1 pr
21	119	6.3	690	2 H86464	hypothetical prote
22	119	6.3	883	2 S04722	puff 74E protein -
23	118.5	6.3	373	2 S43455	hypothetical prote
24	118.5	6.3	500	2 S55785	nucleolar protein
25	118.5	6.3	542	2 S4030	probable membrane
26	117.5	6.2	1537	2 J41172	DNA (cytosine-5-)-
27	117	6.2	534	2 J39903	serine-rich protei
28	117	6.2	720	2 T43327	glucanate transpor
29	117	6.2	2761	2 T21064	hypothetical prote

En/Spm-like transp
proteophosphoglyca
hypothetical prote
HKR1 protein precu
major morozoite su
hypothetical prote
hypothetical prote
hypothetical prote
actin 3 - human (f
actin-interacting
hypothetical prote
major morozoite su
ubiquinol-cytochro
protein-tyrosine-p
disease resistance
hypothetical prote

ALIGNMENTS

RESULT 1

I38659
melanoma antigen MAGE-10 - human
C;Species: Homo sapiens (man)
C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004
C;Accession: I38659
R;De Plaen, E.; Arden, K.; Traversari, C.; Gaforio, J.J.; Szikora, J.P.; De Smet, C.; Bz
oon, T.
Immunogenetics 40, 360-369, 1994
A;Title: Structure, chromosomal localization, and expression of 12 genes of the MAGE fam
A;Reference number: I38659; MUID:95012457; PMID:7927540
A;Accession: I38659
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-369 <RES>
A;Cross-references: UNIPROT:P43363; EMBL:U10685; MID:9533510; PIDN:AAA68869.1; PID:953353
C;Genetics:
A;Gene: GDB:MAGEA10; MAGE10
A;Cross-references: GDB:331126
A;Map position: Xq28-Xq28
A;Introns: #status absent
C;Superfamily: tumor associated protein MAGE

Query Match	Score	DB 1	DB 2	Length	369;
Best Local Similarity	100.0%	Pred. No.	9.6e-122;	Indels	0;
Matches	369;	Conservative	0;	Mismatches	0;
Qy	1	MPRAPKRCMPEDLQSQSETQGLEGAQAPLAVEEDASSSTSTSSFPSSPSSSSSS	60		
Db	1	MPRAPKRCMPEDLQSQSETQGLEGAQAPLAVEEDASSSTSTSSFPSSPSSSSSS	60		
Qy	61	SSCYPLIPSTPEVSADDETPNPQQAQACSSPSVVASLPDQSDGSSSQKEESPSTL	120		
Db	61	SSCYPLIPSTPEVSADDETPNPQQAQACSSPSVVASLPDQSDGSSSQKEESPSTL	120		
Qy	121	QVLPSDESLSRSDIDEKVTDLVQFLFKYQMKPITKAEILSVIKNYEDHFFLLFSEAS	180		
Db	121	QVLPSDESLSRSDIDEKVTDLVQFLFKYQMKPITKAEILSVIKNYEDHFFLLFSEAS	180		
Qy	181	ECMLLVFGIDVKVDPTGHSFVLVTSGLTYDGMVSDVQSMPTGILILSIFIEGYC	240		
Db	181	ECMLLVFGIDVKVDPTGHSFVLVTSGLTYDGMVSDVQSMPTGILILSIFIEGYC	240		
Qy	241	TPEVWEALNMGLVDGMHLLYGEPRKLLTQDWQENYLYRQVPGSPARYEFLWGP	300		
Db	241	TPEVWEALNMGLVDGMHLLYGEPRKLLTQDWQENYLYRQVPGSPARYEFLWGP	300		
Qy	301	RAHAETKMSLLKFLAKVNGSDPRSPPLWYEEERAKDEEERADRIATTTDDTTAMASASS	360		
Db	301	RAHAETKMSLLKFLAKVNGSDPRSPPLWYEEERAKDEEERADRIATTTDDTTAMASASS	360		
Qy	361	ATGFSFSYPE	369		

```
Db 361 ATGSFSYBE 369
|||||
RESULT 2
138660
melanoma antigen MAGE-11 - human
C:Species: Homo sapiens (man)
C:Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004
C:Accession: 138660
R:De Plaen, E.; Arden, K.; Traversari, C.; Gaforio, J.J.; Szikora, J.P.; De Smet, C.; Biondo, T.
Immunogenetics 40, 360-369, 1994
A:Title: Structure, chromosomal localization, and expression of 12 genes of the MAGE family
A:Reference number: 138659; MUID:95012457; PMID:7927540
A:Accession: 138660
A:Molecule type: DNA
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Residues: 1-319 <RES>
A:Cross-references: UNIPROT:P43364; EMBL:U10686; NID:g533512; PIDN:AAA68870.1; PID:g533512
C:Genetics:
A:Gene: GDB:MAGE11; MAGE11
A:Cross-references: GDB:331128
A:Map position: Xg28-Xq28
A:Introns: #status absent
C:Superfamily: tumor associated protein MAGE

Query Match 48.2%; Score 911; DB 2; Length 319;
Best Local Similarity 54.0%; Pred. No. 6.2e-55;
Matches 183; Conservative 53; Mismatches 81; Indels 22; Gaps 2;

Qy 1 MPRAPKRCRCMPEDLQSQETQGLGGAQAPLAVEEDASSSTSTSSPPSPSSSSSS 60
Db 1 MPEQRSHQCKPEGLQAEEDLGLVGAQAQAEQEAFSSST----- 44

Qy 61 SSCYPLPSTPEEVSADDETNPQSAQIACSSPSVVASLPDQSDGSSSQKEESPSTL 120
Db 45 -----LVNGTLEELPA-AESPPSQSQEESFSPPTAMDAIFGSLSDGSGQKEGSPST 98

Qy 121 QVLPDSLSRSEIDEKVTDLVQFLFKYQMKPITKAEILSVIKNYEDHFFLLFSEAS 180
Db 99 PDLIDPESFSQDILHKLIDLVHLLRKRYKGLITKAEMLGSIKNIYEDYFPIFRAS 158

Qy 181 ECLMLVFGIDVKEVDPTGHSFVLVTSGLTYDGMLSDVQSMPTGILILISIFIEGYC 240
Db 159 VCMQLLFGIDVKEVDPTGHSFVLVTSGLTYDGMLSDVQSMPTGILILISIFIEGYC 218

Qy 241 TPEEVIWEALNMGLYDGMELHYGEPRKLLTQDWQENLYEYRQVPGSDPARYEFLLWGP 300
Db 219 IPEEVMWEVLSIMGVYAGREHFLGCEPKRLLTQNNVQSKYLIVYRQVPGTDPACYEFLWGP 278

Qy 301 RAHAETIRKMSLLKFLAKVNGSDPRSPFLMYEALKDDEE 339
Db 279 RAHAETIRKMSLLKFLAKVNGSDPRSPFLMYEALKDDEE 317

RESULT 3
138661
melanoma antigen MAGE-4 - human
N:Alternate names: MAGE 41 protein; melanoma antigen MAGE-X2
C:Species: Homo sapiens (man)
C:Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004
C:Accession: 138661; 138662; PH1297; PH1298; JC2359; G01446
R:De Plaen, E.; Arden, K.; Traversari, C.; Gaforio, J.J.; Szikora, J.P.; De Smet, C.; Biondo, T.
Immunogenetics 40, 360-369, 1994
A:Title: Structure, chromosomal localization, and expression of 12 genes of the MAGE family
A:Reference number: 138659; MUID:95012457; PMID:7927540
A:Accession: 138661
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-317 <DEP1>
A:Cross-references: UNIPROT:P43358; EMBL:U10687; NID:g533514; PIDN:AAA68871.1; PID:g533514
```

```
A:Experimental source: antigen MAGE-4a
A:Accession: 138662
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-172, 'T', 174-317 <DEP2>
A:Cross-references: EMBL:U10688; NID:g533516; PIDN:AAA68872.1; PID:g533517
A:Experimental source: antigen MAGE-4b
R:Traversari, C.; van der Bruggen, P.; Luescher, I.F.; Lurquin, C.; Chomez, P.; Van Pel, J. Exp. Med. 176, 1453-1457, 1992
A:Title: A nonapeptide encoded by human gene MAGE-1 is recognized on HLA-A1 by cytolytic
A:Reference number: PH1294; MUID:93018875; PMID:1402688
A:Accession: PH1297
A:Molecule type: DNA
A:Residues: 169-177 <TRA1>
A:Experimental source: antigen MAGE-4
A:Accession: PH1298
A:Molecule type: DNA
A:Residues: 169-172, 'T', 174-177 <TRA2>
A:Experimental source: antigen MAGE-41
R:Ding, M.; Beck, R.J.; Keller, C.J.; Fenton, R.G.
Biochem. Biophys. Res. Commun. 202, 549-555, 1994
A:Title: Cloning and analysis of MAGE-1-related genes.
A:Reference number: JC2358; MUID:94311935; PMID:8037761
A:Accession: JC2359
A:Molecule type: mRNA
A:Residues: 1-172, 'T', 174-306, 'Q', 308-317 <DIN>
A:Cross-references: EMBL:U10340; NID:g499123; PIDN:AAA19007.1; PID:g499124
A:Experimental source: melanoma cell line DM150
C:Genetics:
A:Gene: GDB:MAGE4; MAGE4; MAGE-X2
A:Cross-references: GDB:331119
A:Map position: Xg28-Xq28
A:Introns: #status absent
C:Superfamily: tumor associated protein MAGE
F:169-177/Region: HLA-A1 binding #status predicted

Query Match 44.9%; Score 849; DB 2; Length 317;
Best Local Similarity 51.6%; Pred. No. 1.1e-50;
Matches 175; Conservative 51; Mismatches 89; Indels 24; Gaps 3;

Qy 1 MPRAPKRCRCMPEDLQSQETQGLGGAQAPLAVEEDASSSTSTSSPPSPSSSSSS 60
Db 1 MSSEQRSHQCKPEGLQAEEDLGLVGAQAQAEQEAFSSSS----- 44

Qy 61 SSCYPLPSTPEEVSADDETNPQSAQIACSSPSVVASLPDQSDGSSSQKEESPSTL 120
Db 45 -----PLVPGTLEELPA-AESAGPPSQSQASALPTTISFTCWQPNEGSSSQKEEGFST- 98

Qy 121 QVLPDSLSRSEIDEKVTDLVQFLFKYQMKPITKAEILSVIKNYEDHFFLLFSEAS 180
Db 99 --SPDAESLFRALSNKVDLAHFLRKRYAKELVTKAEMLERVIKRYKCFPIFGKAS 156

Qy 181 ECLMLVFGIDVKEVDPTGHSFVLVTSGLTYDGMLSDVQSMPTGILILISIFIEGYC 240
Db 157 ESLKMIFFGIDVKEVDPTGHSFVLVTSGLTYDGMLSDVQSMPTGILILISIFIEGYC 216

Qy 241 TPEEVIWEALNMGLYDGMELHYGEPRKLLTQDWQENLYEYRQVPGSDPARYEFLLWGP 300
Db 217 ASSEEIWEELGVMGVGDREHTVYGEPRKLLTQDWQENLYEYRQVPGSDPARYEFLLWGP 276

Qy 301 RAHAETIRKMSLLKFLAKVNGSDPRSPFLMYEALKDDEE 339
Db 277 RALAETSYVKVLEHVVRNARVRIAYPSLREALLDEEE 315

RESULT 4
138668
melanoma antigen MAGE-9 - human
C:Species: Homo sapiens (man)
C:Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004
C:Accession: 138668
R:De Plaen, E.; Arden, K.; Traversari, C.; Gaforio, J.J.; Szikora, J.P.; De Smet, C.; Biondo, T.
```

Immunogenetics 40, 360-369, 1994
A;Title: Structure, chromosomal localization, and expression of the MAGE family of genes
A;Reference number: I38659; MUID:95012457; PMID:7927540
A;Accession: I38668
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-315 <RES>
A;Cross-references: UNIPROT:P43362; EMBL:U10694; NID:g533527; PIDN:AAA68877.1; PID:g533527
C;Genetics:
A;Gene: GDB:MAGEA9; MAGE9
A;Cross-references: GDB:331125
A;Map position: Xp21.3-Xp21.3
A;Introns: #status absent
C;Superfamily: tumor associated protein MAGE

Query Match 44.88; Score 846.5; DB 2; Length 315;
Best Local Similarity 51.08; Pred. No. 1.6e-50;
Matches 172; Conservative 48; Mismatches 88; Indels 29; Gaps 3;

QY 3 RAPKRCRMPEDILQSQETQGLEGAQAPLAVEDASSTSTSSPSPSSSSSSSS 62
DB 6 RSP---HCKPDEDLEAQEDLGLWGAQEPTEGEEETTSSD----- 43

QY 63 CYPLIPSTPREVSADDTNPPOQAQIACSPSVVASLPDQSDGSSSQKESPSSTLQV 122
DB 44 -----SKBEVSAAGSS-SPQSPQGGASSISVYVTLWSQFDEGSSQSEEBEPSSVD 96

QY 123 LPDSESLPRSEIDKVDLQVFLFKYQKPEPTKAILSESVIKNYEDHPLPSEASEC 182
DB 97 PAQLFEFQBALKLVKVAELVHFLHLYRVKPEVTKAEMLESVKNYKRYFPVIFGKASEF 156

QY 183 MLVFGIDVKEVDPTGHSFVLVSLGTYDGMISDVQSMPTKGLILILISIIIFEGYCTP 242
DB 157 MQVIFGTVKEVDPAHSHYILVLTCLGSLGSDGSHMPEKAAALLIIVLGVLTKONCAP 216

QY 243 EEVITWEALNMGLYDGMHEHLYIGEPKLLTQDWQVQENLYRYQVPGSDPARYFELWGP 302
DB 217 EEVITWEALNMGLYDGMHEHLYIGEPKLLTQDWQVQENLYRYQVPGSDPARYFELWGP 276

QY 303 HAETRKMSLLKFLAKVNGSDPRSPPLWVEEALKDEEE 339
DB 277 HAETSYEKVINYLMNARSPICYPISLYEEVLEGEQE 313

RESULT 5
I68889
melanoma antigen MAGE-2 - human
C;Species: Homo sapiens (man)
C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004
C;Accession: I68889; PH1294
R;De Smet, C.; Lurquin, C.; van der Bruggen, P.; De Plaen, E.; Brasseur, F.; Boon, T.
Immunogenetics 39, 121-129, 1994
A;Title: Sequence and expression pattern of the human MAGE2 gene.
A;Reference number: I54519; MUID:94102805; PMID:8276455
A;Accession: I68889
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-314 <RES>
A;Cross-references: UNIPROT:P43356; GB:L18920; NID:g436180; PIDN:AAA17729.1; PID:g436180
R;Traversari, C.; van der Bruggen, P.; Luescher, I.F.; Lurquin, C.; Chomez, P.; Van Pel, J.; Exp. Med. 176, 1453-1457, 1992
A;Title: A nonapeptide encoded by human gene MAGE-1 is recognized on HLA-A1 by cytolytic

QY 1 MRPAPKRCRMPEDILQSQETQGLEGAQAPLAVEDASSTSTSSPSPSSSSSSSS 60
DB 1 MPELQSRQSHQKPEEGLEAGELGLVGAQAPATEQQTASSST----- 44

QY 61 SSCYPLIPSTPREVSADDTNPPOQAQIACSPSVVASLPDQSDGSSSQKESPSSTL 120
DB 45 -----LVEVTLGEVPAAD-SPSPHSPQGGASSISVYVTLWSQFDEGSSQSEEBEPSSVD 95

QY 121 QVLPDSESLPRSEIDKVDLQVFLFKYQKPEPTKAILSESVIKNYEDHPLPSEASEC 180
DB 96 RMFPDLESEFOAAISRKMYELVHFLHLYRVKPEVTKAEMLESVKNYEDHPLPSEASEC 155

QY 181 ECMLLVFGIDVKEVDPTGHSFVLVSLGTYDGMISDVQSMPTKGLILILISIIIFEGYC 240
DB 156 EYLQVFGLEVVEVPIHLYILVLTCLGSLGSDGSHMPEKAAALLIIVLGVLTKONCAP 215

QY 241 TPEVITWEALNMGLYDGMHEHLYIGEPKLLTQDWQVQENLYRYQVPGSDPARYFELWGP 300
DB 216 APEEKIWEELSMLVEFEGREDSVFAHPRKLLMQDLVQENLYRYQVPGSDPARYFELWGP 275

QY 301 RAHAETRKMSLLKFLAKVNGSDPRSPPLWVEEALKDEEE 339
DB 276 RALLETSYVYKVLHHTLTKIGSEPHISYPPPLHERALREGSE 314

RESULT 6
JC2360
melanoma antigen MAGE-6 - human
N;Alternate names: tumor-associated antigen, MAGE-3b
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: JC2360; PH1301; I38665; G01445
R;Ding, M.; Beck, R.J.; Keller, C.J.; Fenton, R.G.
Biochem. Biophys. Res. Commun. 202, 549-555, 1994
A;Title: Cloning and analysis of MAGE-1-related genes.
A;Reference number: JC2358; MUID:94311935; PMID:8037761
A;Accession: JC2360
A;Molecule type: mRNA
A;Residues: 1-314 <DIN>
A;Cross-references: UNIPROT:P43360
A;Experimental source: melanoma cell line DM150
R;Traversari, C.; van der Bruggen, P.; Luescher, I.F.; Lurquin, C.; Chomez, P.; Van Pel, J.; Exp. Med. 176, 1453-1457, 1992
A;Title: A nonapeptide encoded by human gene MAGE-1 is recognized on HLA-A1 by cytolytic

QY 1 MRPAPKRCRMPEDILQSQETQGLEGAQAPLAVEDASSTSTSSPSPSSSSSSSS 60
DB 1 MPELQSRQSHQKPEEGLEAGELGLVGAQAPATEQQTASSST----- 44

QY 61 SSCYPLIPSTPREVSADDTNPPOQAQIACSPSVVASLPDQSDGSSSQKESPSSTL 120
DB 45 -----LVEVTLGEVPAAD-SPSPHSPQGGASSISVYVTLWSQFDEGSSQSEEBEPSSVD 95

QY 121 QVLPDSESLPRSEIDKVDLQVFLFKYQKPEPTKAILSESVIKNYEDHPLPSEASEC 180
DB 96 RMFPDLESEFOAAISRKMYELVHFLHLYRVKPEVTKAEMLESVKNYEDHPLPSEASEC 155

QY 181 ECMLLVFGIDVKEVDPTGHSFVLVSLGTYDGMISDVQSMPTKGLILILISIIIFEGYC 240
DB 156 EYLQVFGLEVVEVPIHLYILVLTCLGSLGSDGSHMPEKAAALLIIVLGVLTKONCAP 215

QY 241 TPEVITWEALNMGLYDGMHEHLYIGEPKLLTQDWQVQENLYRYQVPGSDPARYFELWGP 300
DB 216 APEEKIWEELSMLVEFEGREDSVFAHPRKLLMQDLVQENLYRYQVPGSDPARYFELWGP 275

QY 301 RAHAETRKMSLLKFLAKVNGSDPRSPPLWVEEALKDEEE 339
DB 276 RALLETSYVYKVLHHTLTKIGSEPHISYPPPLHERALREGSE 314

Immunogenetics 40, 360-369, 1994
A;Title: Structure, chromosomal localization, and expression of 12 genes of the MAGE family
A;Reference number: I38659; MUID:95012457; PMID:7927540
A;Accession: I38665
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-314 <RES>
A;Cross-references: EMBL:U10691; NID:g533522; PIDN:AAA68875.1; PID:g533522
R;Fenton, R.G.
submitted to the EMBL Data Library, June 1994
A;Reference number: G0126
A;Accession: G01445
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-314 <FEN>
A;Cross-references: EMBL:U10339; NID:g499121; PIDN:AAA19006.1; PID:g499122
C;Genetics:
A;Gene: GDB:MAGEA6; MAGE6
A;Cross-references: GDB:331121
A;Map position: Xq28-Xq28

```

Qy 1 MPRAPRQRQCMPEEDLOSQSTQGLEGAQAPLAVBEDASSSTSTSSFPSPSSSSSSSS 60
Db 1 MPTLEQRSHQCKPBEGLAEAGEALGLVGAQAPATEEQEAASSST-----44
Qy 61 SSCVPLIPSTPEEVSADDTTPNPQSAQIACSSPVSVASLPL-DQSDGSSSQKEESPST 11
Db 45 -----LVEVTILGEVPA-AESPDPQSPQCASSLPTTM-NYPLWMSQSYEDSSNOEEGFST 97
Qy 120 LQVLPDSESLPRSEIDKQVTDILVQELLFLFYQMKEPITKABILESVIKNYEDHFPLLFSEA 17
Db 98 ---FPDLESSEFOAALSRRKVAELVHFLLLKYRAREPVTKAEMLGSVVGWQYFFPVIFSKA 15
Qy 180 SECMILVFGIDKVEVDPTGHSFVLVTSLSGLTYDGMLSGVQSMPTGILLILLSITFIQY 23
Db 155 SSSLQLVFGIELMEVDPIGHLVIFATCLGSLSYDGLLGDNQIMPKAGLLIIVLAIAREGD 21
Qy 240 CTPEEVIWEALNMGLYDGMELHLYIGEPRKLTQDWQENYLEYRQVPGSDPARYEFLWG 29
Db 215 CAPEEKIWEELSVLVEFEGREDSILGDPKLLTQHFQENYLEYRQVPGSDPACYEFLWG 27
Qy 300 PRAHAIRKMSLLFLAKUNGSDPRSFPPLWYEEALKDEEE 339
Db 275 PRALVETSYVVKLLHVMVKISGGPHISYPPPLHEWVLEEGEE 314

RESULT 8
154519
melanoma antigen Mage-12 - human
N:Alternate names: MAGE 21 protein
C:Species: Homo sapiens (man)
C:Date: 07-Jun-1996 #sequence revision 07-Jun-1996 #text_change 09-Jul-2004
C:Accession: I54519; J02362; PH1295
R:De Smet, C.; Turcotte, C.; van der Bruggen, P.; De Plaen, E.; Brasseur, F.;

```

```
Qy 61 SSCYPLIPSTPEEVSADDETPNPQSAQIACSPSVVASLPLDQSDGSSSQKEESPSTL 120
Db 45 -----LVEVTLREVA-AESPSPHSPQSGASTLPTTINYTLWSQSDGSSNEBQEGPST- 97
Qy 121 QVLPDSESLPRSEIDKVTDLVQFLFKYQMKPEPIKAEILSVIKNYEDHPHLLPSEAS 180
Db 98 --FPDLETSFQVALSRKQWASLVHLLKYLKAREPFTKAEMLGSVIRNFQDFPFVIFSKAS 155
Qy 181 ECLMLVFGIDVKEVDPTGHSFVLVTSGLTYDGMISDVQSMPTKGIILILSLIFIEGYC 240
Db 156 EYLQVFGIEVVEVRIGHLYLVTCGLSYAGLLGDQNIQVPTKGLLIIVLAIKAGDC 215
Qy 241 TPBEVIWEALNMGLYDGMHLYGEPKLLTQDWQENYLEYRQVPGSDPARYEFPLWGP 300
Db 216 APBEKIWEELSVLEASDGRSDVFAHPRKLLTQDLVQENYLEYRQVPGSDPACVEFLWGP 275
Qy 301 RAHAIRKMSLLKFLAKVNGSDPRSFPPLWYEALKDEER 339
Db 276 RALVETSYVKVLHLLKISGPHPIYPPLHEWAFREGGE 314
```

RESULT 9

```
JC2358
melanoma antigen MAGE-1 - human
C/Species: Homo sapiens (man)
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 18-Feb-2000
C/Accession: JC2358
R/Ding, M.; Beck, R.J.; Keller, C.J.; Fenton, R.G.
Biochem. Biophys. Res. Commun. 202, 549-555, 1994
A/Title: Cloning and analysis of MAGE-1-related genes.
A/Reference number: JC2358; MUID:94311935; PMID:8037761
A/Accession: JC2358
A/Molecule type: mRNA
A/Residues: 1-280 <DIN>
A/Experimental source: melanoma cell line DM150
C/Genetics:
C/Supergene: tumor associated protein MAGE
F/161-169/Region: HLA-A1 binding #status predicted
```

```
Query Match 40.5%; Score 766; DB 2; Length 280;
Best Local Similarity 55.1%; Pred. No. 4.2e-45;
Matches 167; Conservative 34; Mismatches 70; Indels 32; Gaps 4;
```

```
Qy 10 CMPEDLQSOSETQGLEGAQAPLAVEEDASSSTSTSSFPSSSSSSSCYPLIPS 69
Db 10 CKPEALAQOALGLVCVA-----ATSSSS-----PLVLG 41
Qy 70 TPEVSADDETPNPQSAQIACSPSVVASLPLDQSDGSSSQKEESPSTLQVLPDSESL 129
Db 42 TLEEVPTAGST-DPPQSPQASAPFTTINFTRQRPSESGSSREEGPSTCIL---ESL 97
Qy 130 PRSEIDKVTDLVQFLFKYQMKPEPIKAEILSVIKNYEDHPHLLPSEASECHMLLVFGI 189
Db 98 FRAVITTKVADLVGFLKLYKAREPFTKAEMLSVKNYKHCPEIFGRKASESLQLVFGI 157
Qy 190 DVKEVDPTGHSFVLVTSGLTYDGMISDVQSMPTKGIILILSLIFIEGYCTPEEVIWEA 249
Db 158 DVKEADPTGHSYLVTCGLSYDGLGDQNIQVPTKGLLIIVLWIANEGGHAREEELWEE 217
Qy 250 LNMGLYDGMHLYGEPKLLTQDWQENYLEYRQVPGSDPARYEFPLWGPRAHAIRKM 309
Db 218 LSNMEVDGHSAYGEPKLLTQDLVQENYLEYRQVDPDPRYEFPLWGPFRALAEYSYV 277
Qy 310 SLL 312
Db 278 KVL 280
```

RESULT 10

```
I38008
melanoma antigen MAGE-B1 - human
N/Alternate names: MAGE-Xp protein; MAGE-like protein 1
```

```
C/Species: Homo sapiens (man)
C/Date: 01-Mar-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
C/Accession: I38008; S52167
R/Muscatelli, P.; Walker, A.P.; De Plaen, E.; Stafford, A.N.; Monaco, A.P.
Proc. Natl. Acad. Sci. U.S.A. 92, 4987-4991, 1995
A/Title: Isolation and characterization of a MAGE gene family in the Xp21.3 region.
A/Reference number: I38008; MUID:95281591; PMID:7761436
A/Accession: I38008
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-347 <RES>
A/Cross-references: UNIPROT:Q96TG1; EMBL:X82539; NID:G608992; PIDN:CAA57889.1; PID:G60899
C/Genetics:
A/Gene: GDB:MAGEB1; MAGEB1; MAGE-Xp
A/Cross-references: GDB:635712; OMIM:600619
A/Map position: Xp21.3-Xp21.3
C/Supergene: tumor associated protein MAGE
```

```
Query Match 38.7%; Score 731; DB 2; Length 347;
Best Local Similarity 42.1%; Pred. No. 1.4e-42;
Matches 157; Conservative 69; Mismatches 115; Indels 32; Gaps 5;
```

```
Qy 1 MRPAPKRCMPEDLQSOSETQGLEGAQAPLAVEEDASSSTSTSSFPSSFPSSSSSS 60
Db 1 MPRGQSKLRAKREKRRKAREETQGLKVRHATAAKBECFSSPVLGDTPTSSPAAG---- 56
Qy 61 SSCYPLIPSTPEEVSADDETPNPQSAQIACSPSVVASLPLDQSDGSSSQKEESPSTL 120
Db 57 -----IPQKPKQ-----GAPPTTAAANVSC-----ESDEGAKCQEEANSPS 94
Qy 121 QVLPDSESLPRSEIDKVTDLVQFLFKYQMKPEPIKAEILSVIKNYEDHPHLLPSEAS 180
Db 95 QATTSTESSVQDPVAWEAGMLHFLIRKYKREPIKADMLKVVDKYLKDHFTTEILNGAS 154
Qy 181 ECLMLVFGIDVKEVDPTGHSFVLVTSGLTYDGMISDVQSMPTKGIILILSLIFIEGYC 240
Db 155 RRLVFGLDLKDNDPSSHTYTLVSKNLNTDGNLNDWDFPRNGLLMPLLVIFLKGNS 214
Qy 241 TPBEVIWEALNMGLYDGMHLYGEPKLLTQDWQENYLEYRQVPGSDPARYEFPLWGP 300
Db 215 ATBEEIWKPNVLGAYDGEHLLYGEPRKFTIQLVQEKYLYEQVNPSPDPYQVFLWGP 274
Qy 301 RAHAIRKMSLLKFLAKVNGSDPRSFPPLWYEALKDEEBRAQDRIAT-----TDDTTAMA 355
Db 275 RAVATTTKKVLEFLAKMGATPRDFPFHYEALRDEEBRAQVRSVRARRRTTATTFFRA 334
Qy 356 SASSSATGFSYP 368
Db 335 RSRAPFSRS-SHP 346
```

RESULT 11

```
I38667
```

```
melanoma antigen MAGE-8 - human
```

```
C/Species: Homo sapiens (man)
```

```
C/Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004
```

```
C/Accession: I38667
```

```
R/De Plaen, E.; Arden, K.; Traversari, C.; Gaforio, J.J.; Szikora, J.P.; De Smet, C.; Bx  
con, T.
```

```
Immunogenetics 40, 360-369, 1994
```

```
A/Title: Structure, chromosomal localization, and expression of the MAGE fam.  
A/Reference number: I38659; MUID:95012457; PMID:7927540
```

```
A/Accession: I38667
```

```
A/Status: preliminary; translated from GB/EMBL/DDBJ
```

```
A/Molecule type: DNA
```

```
A/Residues: 1-234 <RES>
```

```
A/Cross-references: UNIPROT:P43361; EMBL:U10693; NID:G533525; PIDN:AAA68876.1; PID:G533525
```

```
C/Genetics:
```

```
A/Gene: GDB:MAGEA8; MAGE8
```

```
A/Cross-references: GDB:331123
```

```
A/Map position: Xq28-Xq28
```

```
A/Introns: #status absent
```

```
C/Supergene: tumor associated protein MAGE
```


A/Accession: PH1300
A/Molecule type: DNA
A/Residues: 125-133 <TRA2>
A/Experimental source: MAGE 51 protein
C/Genetics:
A/Gene: GDB:MAGEA5; MAGE5
A/Cross-references: GDB:331120
A/Map position: Xq28-Xq28
A/Introns: #status absent
C/Superfamily: tumor associated protein MAGE

Query Match 11.8%; Score 222.5; DB 2; Length 133;
Best Local Similarity 39.3%; Pred. No. 1.9e-08;
Matches 57; Conservative 19; Mismatches 44; Indels 25; Gaps 3;
Qy 6 KRQCMPEEDLQSQETQGLEGAQPLAVEDEDASSSTSSPPSPSSSSSSSSSCYP 65
Db 6 KSHCKPFRGLDTQEEALGLVGQAATTEQEAIVSSSS-----P 44
Qy 66 LIPSTPEVSADDETPNPQSAQIACSPSVVASLPLDQSDGSSQKESPSSTLQVLPD 125
Db 45 LVPCTLGEVPAAG-SPGPLKSPQASAIPTAIDTLWRQSIKGSNNQEEGPST---SPD 100
Qy 126 SESLPRSEIDEKVTDLVQFLFKYQ 150
Db 101 PESVFRAALSKKVADLIHFLLLKYE 125

RESULT 15
Til1678
hypothetical protein SPBC21D10.06c - fission yeast (Schizosaccharomyces pombe)
C/Species: Schizosaccharomyces pombe
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C/Accession: Til1678
R/Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, September 1998
A/Reference number: Z17313
A/Accession: Til1678
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-948 <SEE>
A/Cross-references: UNIPROT:O74346; EMBL:AL031536; NID:e1319499; PID:e1319505
A/Experimental source: strain 972h(-)
C/Genetics:
A/Map position: IIR
A/Note: SPBC21D10.06c

Query Match 6.7%; Score 126.5; DB 2; Length 948;
Best Local Similarity 20.8%; Pred. No. 0.94;
Matches 84; Conservative 56; Mismatches 138; Indels 125; Gaps 18;
Qy 16 LOSQSETQGLEGAQPLAVEDEDASSSTST-----SSSPSPSP-----SSSSSSSSSCYP 65
Db 237 LESSLNTVSGTSTPYETKSTSSVPTQIDSSFTSTPVSFLTSSSTSSSSSQDST 296
Qy 66 LIPSTPEVSADDETPNPQSAQIACSPSVVASLPLDQSDGSSQKESPSSTLQVLPD 125
Db 297 TIDSTPIAT--STLQPTTSSPITTSAPLSALPTY-----PSSLSTEVE 342
Qy 126 SESLPRSEIDEKVTDLVQFLFKYQK-----EPITKAEILESIVKYNEDHFLFSEAS 180
Db 343 VEYFTKT-----ITDTSIVTYSTGVETLYETETITSSEI-SSIIYNFST--PISSGS-- 392
Qy 181 ECLLVFGIDVKEVDPTCHSFVLVTSGLTYDGMLSDVQSMPTGI----- 226
Db 393 -----FPDGFKPINPT-----SPSLTSTTKKIPSTTLPTSSKMITTTTSPV 434
Qy 227 -----LILILSIIFEGYCTPEEVIWEALNMGILYDGMHLLYGEPRKLLTQDWQENY 280
Db 435 SNNTQSSFLIIS--TFTSY-----EH---SEPFKVSVPVLTNNP 470
Qy 281 LEYRQVPGSD-----PARYEFLWGPRAHAEIRKMLLKLAKY-----NGSDP-- 323

471 SSISHSSASSLPITPSSY--LSNTTLHSSVQSSSQSQFTVSPSPSTQSVSTSGNFTTPT 528
324 -----RSFPLWYEEALKDEBERAODRIATDDTTAMASASSSA 361
529 ISTSLSPFTTIVSSSFQYSSLSLSSNTVTTTNAQSSLSLSSNSA 571

Search completed: November 15, 2005, 15:44:44
Job time : 53.7381 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 15, 2005, 15:31:39 ; Search time 215.738 Seconds
(without alignments)
875.864 Million cell updates/sec

Title: US-09-856-812b-1

Perfect score: 1891

Sequence: 1 MPRAPKRCQRCPEEDLQSQS.....DTTAMASASSATGFSFSYPE 369

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1891	100.0	369	1	MAGA HUMAN
2	911	48.2	319	1	MAGA HUMAN
3	910	48.2	394	2	Q6ZR25
4	911	48.1	318	2	Q9BUN9
5	854	45.2	317	1	MAGA HUMAN
6	846.5	44.8	315	1	MAG9_HUMAN
7	846.5	44.8	315	2	Q7Z5K4
8	828	43.8	378	2	Q9TTY4
9	827	43.7	317	2	Q14798
10	813	43.0	346	2	Q9IZ00
11	812	42.9	346	1	MG2A HUMAN
12	811.5	42.9	316	2	Q9WHG6
13	807	42.7	309	1	MAG1 HUMAN
14	806.5	42.6	314	2	Q96E03
15	804.5	42.5	314	2	Q9P448
16	800.5	42.3	314	1	MAG2 HUMAN
17	800.5	42.3	314	2	Q9FGT7
18	798.5	42.2	314	1	MAG6_HUMAN
19	794.5	42.0	314	2	Q6FH15
20	793	41.9	346	2	Q7L852
21	792.5	41.9	314	2	Q6NW44
22	790.5	41.8	314	1	MAGC HUMAN
23	793.5	41.4	314	1	MAG3_HUMAN
24	765	40.5	373	1	MG2C_HUMAN
25	765	40.5	373	2	Q6IAI7
26	760.5	40.2	347	2	Q96LZ2
27	748	39.6	1142	1	MG1C1_HUMAN
28	742	39.2	347	1	MGB1_HUMAN
29	742	39.2	347	2	Q6FHJ0
30	739	39.1	320	2	Q99009
31	736	38.9	343	2	Q96M61

32	731	38.7	347	2	Q96TG1
33	718	38.0	320	2	Q89007
34	718	38.0	347	2	Q96CW8
35	717	37.9	320	2	Q6T340
36	717	37.9	429	2	Q9D4D2
37	716	37.9	315	2	Q89008
38	714	37.8	325	2	Q89010
39	711	37.6	320	2	Q89012
40	702	37.1	311	2	Q9BG82
41	702	37.1	320	2	Q89006
42	699	37.0	320	2	Q9R2A2
43	674	35.6	360	2	Q6AY37
44	668	35.3	363	2	Q9CWV4
45	667	35.3	303	2	Q8BQJ2

ALIGNMENTS

RESULT 1

ID	MAGA HUMAN	STANDARD	PRT	369 AA
AC	P43363			
DT	01-NOV-1995 (Rel. 32, Created)			
DT	01-NOV-1995 (Rel. 32, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Melanoma-associated antigen 10 (MAGE-10 antigen).			
GN	Name=MAGEA10; Synonyms=MAGE10;			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Theria; Primates; Catarrhini; Hominoidea; Homo.			
OX	NCBI_TaxID:9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=95012457; PubMed=7927540;			
RA	de Plaen E., Arden K., Traversari C., Gaforio J.J., Szikora J.-P.,			
RA	de Smet C., Brasseur F., van der Bruggen P., Ietche B., Lurquin C.,			
RA	Brasseur R., Chomez P., de Backer O., Cavenee W., Boon T.;			
RT	"Structure, chromosomal localization, and expression of 12 genes of			
RT	the MAGE family."			
RL	Immunogenetics 40:360-369(1994).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Skin;			
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,			
RA	Klausner R.D., Collins P.S., Wagner L., Shennan C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Udén T.B., Tohiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,			
RA	Schneerch A., Schein J.E., Jones S.J.M., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences."			
PL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
CC	-!- FUNCTION: Not known, though may play a role in embryonal			
CC	development and tumor transformation or aspects of tumor			
CC	progression.			
CC	-!- TISSUE SPECIFICITY: Expressed in many tumors of several types,			
CC	such as melanoma, head and neck squamous cell carcinoma, lung			
CC	carcinoma and breast carcinoma, but not in normal tissues except			
CC	for testes and placenta.			
CC	-!- SIMILARITY: Contains 1 MAGE domain.			

```

CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U10685; AAA688670.1; -.
DR EMBL; BC0044105; AAH04479.1; -.
DR PIR; I38659; I38659.
DR Genew; HGNC:6797; MAGEA10.
DR H-InvDB; HIX0017116; -.
DR MIM; 300343; -.
DR InterPro; IPR002190; MAGE.
DR Pfam; PF01454; MAGE; 1.
DR PROSITE; PS50838; MAGE; 1.
KW Antigen; Multigene family; Tumor antigen.
FT DOMAIN 134 333
FT DOMAIN 54 62 Poly-Ser.
SQ SEQUENCE 369 AA; 40766 MW; 16FA3301CAB716A6 CRC64;
Query Match 100.0%; Score 1891; DB 1; Length 369;
Best Local Similarity 100.0%; Pred. No. 1e-115;
Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY { 1 MPRAKQRCMPEDLQSQSETQGLGQAQAPLAVEEDASSSTSTSSFPSPSSSSSS 60
Db { 1 MPRAKQRCMPEDLQSQSETQGLGQAQAPLAVEEDASSSTSTSSFPSPSSSSSS 60
QY 61 SSCYPLIPSTPEEVASDDETPNPQSAQIACSSPSVVASLPDQSDGSSSQKESPSSTL 120
Db 61 SSCYPLIPSTPEEVASDDETPNPQSAQIACSSPSVVASLPDQSDGSSSQKESPSSTL 120
QY 121 QVLPDSLSRSEIDKVTDLVQVLLFKYQKKEPTTKAEILLESVKNYEDHFFLLFSEAS 180
Db 121 QVLPDSLSRSEIDKVTDLVQVLLFKYQKKEPTTKAEILLESVKNYEDHFFLLFSEAS 180
QY 181 ECLMLVFGIDVKEVDPTGHSFVLVTSGLTYDGMLSVQSMKPTGILLIILSIPIEGYC 240
Db 181 ECLMLVFGIDVKEVDPTGHSFVLVTSGLTYDGMLSVQSMKPTGILLIILSIPIEGYC 240
QY 241 TPEEVIALNMGLYDGMHLYIGEPRKLLTQDWQENLYEYRQVPGSDPARYEFLLWGP 300
Db 241 TPEEVIALNMGLYDGMHLYIGEPRKLLTQDWQENLYEYRQVPGSDPARYEFLLWGP 300
QY 301 RAHAERIKWSLLKFLAKVNGSDPRFPLWYBEALKDEERAAQDRITATDDTTAMASASS 360
Db 301 RAHAERIKWSLLKFLAKVNGSDPRFPLWYBEALKDEERAAQDRITATDDTTAMASASS 360
QY 361 ATGSFSYPE 369
Db 361 ATGSFSYPE 369
RESULT 2
MAGE_HUMAN
ID MAGE_HUMAN STANDARD; PRT; 319 AA.
AC P43364;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Melanoma-associated antigen 11 (MAGE-11 antigen).
GN Name=MAGE11; Synonyms=MAGE11;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95012457; PubMed=7927540;
RA de Plaen E., Arden C., Traversari C., Gaforio J.J., Szikora J.-P.,

```

```

RA de Smet C., Brasseur F., van der Bruggen P., Lethe B., Lurquin C.,
RA Brasseur R., Chomez P., de Backer O., Cavenee W., Boon T.;
RT "Structure, chromosomal localization, and expression of 12 genes of
RL the MAGE family.";
RN Immunogenetics 40:360-369 (1994).
RC [2]
RC SEQUENCE FROM N.A.
RC TISSUE=Skin;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -!- FUNCTION: Not known, though may play a role in embryonal
CC development and tumor transformation or aspects of tumor
CC progression.
CC -!- TISSUE SPECIFICITY: Expressed in many tumors of several types,
CC such as melanoma, head and neck squamous cell carcinoma, lung
CC carcinoma and breast carcinoma, but not in normal tissues except
CC for testes and placenta.
CC -!- SIMILARITY: Contains 1 MAGE domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U10686; AAA68870.1; -.
DR EMBL; BC004479; AAH04479.1; -.
DR PIR; I38660; I38660.
DR Genew; HGNC:6798; MAGEA11.
DR H-InvDB; HIX0022316; -.
DR MIM; 300344; -.
DR InterPro; IPR002190; MAGE.
DR Pfam; PF01454; MAGE; 1.
DR PROSITE; PS50838; MAGE; 1.
KW Antigen; Multigene family; Tumor antigen.
FT DOMAIN 112 311
FT DOMAIN 319 AA; 35536 MW; F51A0B4140277BE3 CRC64;
SQ SEQUENCE 319 AA; 35536 MW; F51A0B4140277BE3 CRC64;
Query Match 48.2%; Score 911; DB 1; Length 319;
Best Local Similarity 54.0%; Pred. No. 1.1e-51;
Matches 183; Conservative 53; Mismatches 81; Indels 22; Gaps 2;
QY 1 MPRAKQRCMPEDLQSQSETQGLGQAQAPLAVEEDASSSTSTSSFPSPSSSSSS 60
Db 1 MPLEQRSQCHKPEGLQAQEDLGLVGAQALQAEQEAFFSST----- 44
QY 61 SSCYPLIPSTPEEVASDDETPNPQSAQIACSSPSVVASLPDQSDGSSSQKESPSSTL 120
Db 45 -----LNVGTLIELPA-AESFSPQSPQESFSTAMDAIFGSLSDGSGSQEKGST 98
QY 121 QVLPDSLSRSEIDKVTDLVQVLLFKYQKKEPTTKAEILLESVKNYEDHFFLLFSEAS 180

```

```
Db 99 POLIDPESFSDILHDKIIDLVLHLLRKYRVKGLITKAEMLGSVIKNYEDYFPEIPREAS 158
Qy 181 ECVLLVFGIDVKEVDPTGHSFVLVTSGLTVDGMLSDVQSMPTKGIILILSIFIRGYC 240
Db 159 VCMQLLFGIDVKEVDPTGHSFVLVTSGLTVDGMLSDVQSMPTKGIILILSIFIRGYC 218
Qy 241 TPEVIVWALMMGLDGMHLYIGEPKRLTQDWQENLYEYQVPGSPDARYEFLWGP 300
Db 219 IPEVIVWALMMGLDGMHLYIGEPKRLTQDWQENLYEYQVPGSPDARYEFLWGP 278
Qy 301 RAHAERIKMSLLKFLAKVNGSDPRSFPPLWYEEALKDREE 339
Db 279 RAHAETSKMKVLEYIANANGRDPTSYPSLYEDALRBEGE 317

RESULT 3
Q6ZR25 PRELIMINARY; PRT; 394 AA.
AC Q6ZR25;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Hypothetical protein FLJ45952.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Tachiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S.,
RA Fukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R.,
RA Otaki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
RA Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A.,
RA Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K.,
RA Isogai T.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK127849; BAC97161.1; -.
DR InterPro; IPR002190; MAGE.
DR Pfam; PF01454; MAGE; 1.
DR PROSITE; PS00838; MAGE; 1.
SQ SEQUENCE 394 AA; 44276 MW; 36D7A81D8749D896 CRC64;

Query Match 48.2%; Score 911; DB 2; Length 394;
Best Local Similarity 54.0%; Pred. No. 1.5e-51;
Matches 183; Conservative 53; Mismatches 81; Indels 22; Gaps 2;

Qy 1 MPRAKPRQCMPEEDLQSQETQGLGAQAPLAVEEDASSSTSTSSSPSPSPSSSSSS 60
Db 76 MPLEQRQHQCKPEGLQAEEDLGLVQAQALQAEQEAAPFSST----- 119

Qy 61 SSCVPLIPSTPEEVSADDETNPQSQAIACSSPSVVASLPDQSDGSSSQKEESPSTL 120
Db 120 -----LNVGTLEELPA-AEESPSPQSEFSPTAMDALFGLSGSGSQKEGPGSTS 173

Qy 121 QVLPDSLSLPRSEIDEXVTDLVQFLPKYQWKEPITKATILESIVKNYEDHFFLLPSEAS 180
Db 174 PDLIDPESFSDILHDKIIDLVLHLLRKYRVKGLITKAEMLGSVIKNYEDYFPEIPREAS 233

Qy 181 ECVLLVFGIDVKEVDPTGHSFVLVTSGLTVDGMLSDVQSMPTKGIILILSIFIRGYC 240
Db 234 VCMQLLFGIDVKEVDPTGHSFVLVTSGLTVDGMLSDVQSMPTKGIILILSIFIRGYC 293

Qy 241 TPEVIVWALMMGLDGMHLYIGEPKRLTQDWQENLYEYQVPGSPDARYEFLWGP 300
Db 294 IPEVIVWALMMGLDGMHLYIGEPKRLTQDWQENLYEYQVPGSPDARYEFLWGP 353

Qy 301 RAHAERIKMSLLKFLAKVNGSDPRSFPPLWYEEALKDREE 339
Db 354 RAHAETSKMKVLEYIANANGRDPTSYPSLYEDALRBEGE 392
```

RESULT 4

```
Q9BUN9 PRELIMINARY; PRT; 318 AA.
AC Q9BUN9;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DB Melanoma antigen, family A, 8.
GN Name=MAGEA8;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
RA Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalak U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Kalnine N., Chen X., Rolfe A., Halleck A., Hines L., Eisenstein S.,
RA Koundinya M., Raphael J., Moreira D., Kelley T., Labaer J., Lin Y.,
RA Phelan M., Farmer A.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Strausberg R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002455; AAH02455.1; -.
DR EMBL; BT007340; AAP36004.1; -.
DR EMBL; BC012744; AAH12744.1; -.
DR InterPro; IPR002190; MAGE.
DR Pfam; PF01454; MAGE; 1.
DR PROSITE; PS00838; MAGE; 1.
SQ SEQUENCE 318 AA; 35214 MW; EA02C1FB42F6C080 CRC64;

Query Match 48.1%; Score 910; DB 2; Length 318;
Best Local Similarity 56.5%; Pred. No. 1.3e-51;
Matches 186; Conservative 45; Mismatches 78; Indels 22; Gaps 2;

Qy 6 KRQRCMPEEDLQSQETQGLGAQAPLAVEEDASSSTSTSSSPSPSPSSSSSSSCYP 65
Db 6 KSRQRYAEGLQAQGEAPGLMDVQIPTAEERQAASST----- 44

Qy 66 LIPSTPEEVSADDETNPQSQAIACSSPSVVASLPDQSDGSSSQKEESPSTLQVLPD 125
Db 45 LIMGTLEEVTDGSGSPSPQSPGAGSSLTVTDTLWSQSDGSSNEEGSPSTSPDPAH 103
```



```
RESULT 6
MAG9 HUMAN STANDARD; PRT; 315 AA.
AC P43362, Q92910;
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Melanoma-associated antigen 9 (MAGE-9 antigen).
GN Name=MAGEA9; Synonyms=MAGE9;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=95012457; PubMed=7927540;
RA de Plaen E., Arden K., Traversari C., Gaforio J.J., Szikora J.-P.,
RA de Smet C., Brasseur F., van der Bruggen P., Lethe B., Lurquin C.,
RA Brasseur R., Chomez P., de Backer O., Cavenee W., Boon T.;
RT "Structure, chromosomal localization, and expression of 12 genes of
RT the MAGE family.";
PL Immunogenetics 40:360-369(1994).
RN [2]
SEQUENCE FROM N.A.
RX Timms K.M., Bondeson M.L., Ansari-Lari M.A., Lagerstedt K.,
RA Nelson D.L., Pettersson U., Gibbs R.A.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Heish F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ussid T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bonak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinstead J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
PL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Not known, though may play a role in embryonal
CC development and tumor transformation or aspects of tumor
CC progression.
CC -!- TISSUE SPECIFICITY: Expressed in many tumors of several types,
CC such as melanoma, head and neck squamous cell carcinoma, lung
CC carcinoma and breast carcinoma, but not in normal tissues except
CC for testes and placenta.
CC -!- SIMILARITY: Contains 1 MAGE domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U10694; AAA68877.1; -
CC EMBL; U66083; AAA67888.1; -
CC PIR; I38668; I38668.
CC Genew; HGNC:6807; MAGEA9.
CC -----
DR H-InvDB; HIX0017105; -
DR MIM; 300342; -
DR InterPro; IPR002190; MAGE.
DR Pfam; PF01454; MAGE; 1.
DR PROSITE; PS0838; MAGE; 1.
KW Antigen; Multigene family; Tumor antigen.
FT DOMAIN 108 307 MAGE.
FT DOMAIN 34 37 Poly-Glu.
FT DOMAIN 87 90 Poly-Glu.
SQ SEQUENCE 315 AA; 35088 MW; 7FD2ED10D680D928 CRC64;
Query Match 44.8%; Score 846.5; DB 1; Length 315;
Best Local Similarity 51.0%; Pred. No. 1.8e-47;
Matches 172; Conservative 48; Mismatches 88; Indels 29; Gaps 3;
QY 3 RAPKRCMPEDLQSQETQGLEGAQAPLAVDEDASSSTSTSSPSSPSSSSSSSSSS 62
DB 6 RSP---HCRPDELEAAGDGLMGAGQEPGGEETSSD----- 43
QY 63 CYELIPTPEVSGADDETPNPQSAQIACSSPSVASLPDQSDGSSSQKESPSSTLQV 122
DB 44 -----SKEEVSAAGSS-SPQSPQSGASSISVYVTLWSQFDEGSSSQEETSSSD 96
QY 123 LPDSLSLRSEIDEKVTDLVQFLFKYKMKPPTKAIKLESVKYKVEDHPFLFSEASEC 182
DB 97 PAQLLEFMFOEALKLVKVAELVHLLHKYRKVPVTKAEMLESVKYKRPVIFGKASEF 156
QY 183 MLVFGIDVKEVDPTGHSFVLVTSGLTYDGMISDVQSPKPTGILILILSIFIEGYCTP 242
DB 157 MQVIFGTDVKEVDPAHSGSVLTVLGLSCDSMLGDGSHMPKAAALLIIVGLVITKNCAP 216
QY 243 EEVIEALNMGLYDGMHLLIYGEPRKLLTQDWVQENLYEYRQVPGSDPARYFLWGPRA 302
DB 217 EEVIEALSVMGVYVYKHEMFYGEPRKLLTQDWVQENLYEYRQVPGSDPARYFLWGSKA 276
QY 303 HAEIRKMSLLKFLAKVNGSDPRSPFLPYEALKDEEE 339
DB 277 HAETSEYKVINYLMLNAREPICYPISLYEVLGEEQE 313
RESULT 7
Q725K4 PRELIMINARY; PRT; 315 AA.
AC Q725K4;
DT 01-OCT-2003 (T-EMBLrel. 25, Created)
DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Melanoma antigen family A 9 (fragment).
GN Name=MAGEA9;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Zhu J., Feng Z., Guan X.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY310325; AAP82171.1; -
DR InterPro; IPR002190; MAGE.
DR Pfam; PF01454; MAGE; 1.
DR PROSITE; PS0838; MAGE; 1.
FT NON TER 315 315
SQ SEQUENCE 315 AA; 35116 MW; C9488470D409B96F CRC64;
Query Match 44.8%; Score 846.5; DB 2; Length 315;
Best Local Similarity 51.0%; Pred. No. 1.8e-47;
Matches 172; Conservative 48; Mismatches 88; Indels 29; Gaps 3;
QY 3 RAPKRCMPEDLQSQETQGLEGAQAPLAVDEDASSSTSTSSPSSPSSSSSSSSSS 62
DB 6 RSP---HCRPDELEAAGDGLMGAGQEPGGEETSSD----- 43
```

```

Qy 63 CVPLIPSTPEEVSADDETPNPQSAQIACSSPVVASLPDQSDGSSQKEESPSTLQV 122
Db 44 -----SKEEEVSAGSS-SPQSPQCGAGSSISVYTLWQFDEGSSSQEGEPSSSVD 96

Qy 123 LPDSESLPRSEIDEKVDLQVFLPKYQKBPITKAEILSVIKNYEDHFFLFFSEASEC 182
Db 97 PAQLEFMFOEALKLVAELVHFLHKKYRGVPVTKAEMLESVKNYKRYFFVIFGKASEF 156

Qy 183 MLLVFGIDVKEVDPTGHSFVLVTSGLTYDGMLSVQSMPTGILILILISLIFEGYCTP 242
Db 157 MOVIFGTVDVKEVDPAHSGYIILVTALGLSCDMLGDSHSMKPAALIIIVLVTKNDCAP 216

Qy 243 BEVIWEALNMGLYDGMHLYGEBRKLITQDWQENYLEYRQVPGSDPARVEFLWGPRA 302
Db 217 BEVIWEALNVGMYGVYKEMHYGEBRKLITQDWQENYLEYRQVPGSDPARVEFLWGSKA 276

Qy 303 HAEIRKMSLLKFLAKVNGSDPRSPFLWYEALKDDEE 339
Db 277 HAETSVEKVINVLNAREPICVPSLYEEVLEEE 313

RESULT 8
Q9TTY4
ID Q9TTY4 PRELIMINARY; PRT; 378 AA.
AC Q9TTY4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Melanoma antigen.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=beed beagle; TISSUE=Testis;
RX MEDLINE=20470598; PubMed=11019919;
RA Ma Z., Khatlani T.S., Ohno K., Sasaki K., Inokuma H., Onishi T.;
RT "Cloning and sequencing of canine MAGE CDNA.";
RL Tissue Antigens 56:166-169(2000).
DR EMBL; AF187325; AAF01438.1; -.
DR InterPro; IPR002190; MAGE.
DR Pfam; PF01454; MAGE; 1.
DR PROSITE; PS50838; MAGE; 1.
SQ SEQUENCE 378 AA; 42214 MW; AD09C6DC9E3C8D57 CRC64;

Query Match 43.8%; Score 828; DB 2; Length 378;
Best Local Similarity 49.2%; Pred. No. 3.8e-46;
Matches 179; Conservative 52; Mismatches 107; Indels 26; Gaps 3;

Qy 1 MPRAPKRCMPEDLQSQSETQGLEGAQAPLAVEDASSSTSTSSPSSPSSSSSSSS 60
Db 1 MPRGQSKLRACKRRQVRELDLVGAQAATAAAGEVFHSPSSL--CFKSS-PAAGSYSV 57

Qy 61 SSCYPLIPSTPEEVSADDETPNPQSAQIACSSPVVASLPDQSDGSSQKEESPSTL 120
Db 58 S-----QGPGALSTSTTAASVHSTRSNESADNQVERPRSS 94

Qy 121 QVLDPSESLPRSEIDEKVDLQVFLPKYQKBPITKAEILSVIKNYEDHFFLFFSEAS 180
Db 95 QAOPTAEPFRGRLDEKVKVLLVHLLYKYQKELISKAGMLRNVTQMYRNFHFLKRAAS 154

Qy 181 ECLLVFGIDVKEVDPTGHSFVLVTSGLTYDGMLSVQSMPTGILILILISLIFEGYC 240
Db 155 EHLELVFGDLDEVDPNRHIIYVLNKLSELYDAMLSDDGVPKTLGLMTIILGVTIKNC 214

Qy 241 TPEVIWEALNMGLYDGMHLYGEBRKLITQDWQENYLEYRQVPGSDPARVEFLWGP 300
Db 215 AAEQVMQVNLVIGLYACMEHFIFGEBRKLITDLVKEYLEYRQVNSDPRVEFLWGP 274

Qy 301 RAHAEIRKMSLLKFLAKVNGSDPRSPFLWYEALKDDEERAQDIATDDTTMASASSS 360
Db 275 RAYAEISKMKVLEFLAKVHYTVPSAFPAYWEALQDEERAQAAAAAHTAANASARAR 334

```

```

Qy 361 ATGS 364
Db 335 AMTS 338

RESULT 9
Q14798
ID Q14798 PRELIMINARY; PRT; 317 AA.
AC Q14798;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE MAGE-4 protein.
OS Name=melanoma antigen-4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95369706; PubMed=7642112; DOI=10.1016/0378-1119(94)00680-Q;
RA Imai Y., Shichiyo S., Yamada A., Katayama T., Yano H., Itoh K.;
RT "Sequence analysis of the MAGE gene family encoding human tumor-
rejection antigens.";
RL Gene 160:287-290(1995).
DR EMBL; D32075; BAA06841.1; -.
DR InterPro; IPR002190; MAGE.
DR Pfam; PF01454; MAGE; 1.
DR PROSITE; PS50838; MAGE; 1.
SQ SEQUENCE 317 AA; 35044 MW; 9B9477253FE307C4 CRC64;

Query Match 43.7%; Score 827; DB 2; Length 317;
Best Local Similarity 51.2%; Pred. No. 3.5e-46;
Matches 171; Conservative 53; Mismatches 86; Indels 24; Gaps 3;

Qy 6 KRORCMPEEDLQSQSETQGLEGAQAPLAVEDASSSTSTSSPSSPSSSSSSSSCYP 65
Db 6 KSQCKPEEGVEAQEEALGLVGAQPTTEQEAASVSSS-----P 45

Qy 66 LIPSTPEEVSADDETPNPQSAQIACSSPVVASLPDQSDGSSQKEESPSTLQVLPD 125
Db 46 LVLGTLEKVPAA-AESADPPQSQASALPTTISFTCWRQPNEGSSSQEESSEAST---SPD 101

Qy 126 SESLPRSEIDEKVDLQVFLPKYQKBPITKAEILSVIKNYEDHFFLFFSEASECMLL 185
Db 102 AESLFRALSNKYDELAAHFLLRKYRAKBLVTKAEMLESVKNYKRCFPVIFGKASESLKM 161

Qy 186 VFGIDVKEVDPTGHSFVLVTSGLTYDGMLSVQSMPTGILILILISLIFEGYCTPEEV 245
Db 162 IFGIDVKEVDPAASNTYTLVTLGLSYDGLGNQIFPKTGLLIIVLGTIAMEGDSASEEE 221

Qy 246 IWEALNMGLYDGMHLYGEBRKLITQDWQENYLEYRQVPGSDPARVEFLWGPRAHAE 305
Db 222 IWEELGVNGVYDGRHTVYGEPRKLITQDWQENYLEYRQVPGSNPARVEFLWGPRAAE 281

Qy 306 IRKMSLLKFLAKVNGSDPRSPFLWYEALKDDEE 339
Db 282 TSYVKVLEHVVRNARVRIAYPSLREAALEEE 315

RESULT 10
Q81200
ID Q81200 PRELIMINARY; PRT; 346 AA.
AC Q81200;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Melanoma antigen, family B, 4.
OS Name=MAGEB4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```


GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 15, 2005, 15:33:16 ; Search time 59.5476 Seconds
(without alignments)
462.579 Million cell updates/sec

Title: US-09-856-812B-1

Perfect score: 1891

Sequence: 1 MPRAPKQRQWPEEDLQSQS.....DTTAMASASSATCSFSYPE 369

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PTOS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1891	100.0	369	2	US-08-773-870-4
2	911	48.2	319	4	US-09-949-016-8188
3	807	42.7	309	1	US-08-465-167A-24
4	807	42.7	309	2	US-08-993-118-10
5	807	42.7	309	3	US-08-845-528C-10
6	807	42.7	309	4	US-08-627-820-24
7	807	42.7	309	4	US-09-066-281B-10
8	807	42.7	309	4	US-09-468-433C-10
9	807	42.7	309	4	US-09-392-714-29
10	807	42.7	309	4	US-09-949-016-6574
11	807	42.7	355	4	US-09-949-016-8559
12	793	41.9	345	4	US-09-468-433C-22
13	783.5	41.4	314	2	US-08-928-615-2
14	783.5	41.4	314	3	US-09-166-448-2
15	783.5	41.4	314	3	US-09-348-933-2
16	783.5	41.4	314	4	US-09-697-884-2
17	783.5	41.4	314	4	US-09-392-714-30
18	783.5	41.4	314	4	US-09-396-315-2
19	783.5	41.4	314	4	US-09-849-602-29
20	765	40.5	373	4	US-09-066-281B-19
21	765	40.5	373	4	US-09-468-433C-19
22	760	40.2	312	4	US-09-949-016-9310
23	748	39.6	1142	2	US-08-993-118-7
24	748	39.6	1142	3	US-08-845-528C-7
25	748	39.6	1142	3	US-09-061-709-2
26	748	39.6	1142	4	US-09-066-281B-7
27	748	39.6	1142	4	US-09-899-651-2

Sequence 7, Appli
Sequence 26, Appli
Sequence 2, Appli
Sequence 11171, A
Sequence 11172, A
Sequence 3, Appli
Sequence 8202, Ap
Sequence 26, Appli
Sequence 5, Appli
Sequence 24, Appli
Sequence 6, Appli
Sequence 6944, Ap
Sequence 11308, A
Sequence 2, Appli
Sequence 1, Appli
Sequence 6, Appli
Sequence 6400, Ap

ALIGNMENTS

RESULT 1
US-08-773-870-4
; Sequence 4, Application US/08773870
; Patent No. 5912143
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL HUMAN MAGE-LIKE PROTEIN
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/773,870
; FILING DATE: Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0179 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 369 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 533511
US-08-773-870-4

Query Match 100.0%; Score 1891; DB 2; Length 369;
Best Local Similarity 100.0%; Pred. No. 1.2e-172;
Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


```
Db 278 KLEVYIKVSARVRFPPSLREAAALREEE 307

RESULT 10
US-09-949-016-6574
; Sequence 6574, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6574
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6574

Query Match 42.7%; Score 807; DB 4; Length 309;
Best Local Similarity 53.6%; Pred. No. 7.6e-69;
Matches 177; Conservative 40; Mismatches 81; Indels 32; Gaps 4;

Qy 10 CMPEEDLOSQSETQGLEGAQAPLAVEEDASSSTSTSSFFSPSSSSSSSSSCYPLIPS 69
Db 10 CKPEALEAQOALGLVCQA-----ATSSSS-----PLVLG 41
Qy 70 TPEVSADDETPNPQSAQIACSPSVASLPDQSDGSSSOKESPSSTLQVLDPDSLSL 129
Db 42 TLEEVPTAGST-DPPQSPQASAFPTTINFRQPSGSSSREEGPSTSCIL---ESL 97
Qy 130 PRSEIDEKVTDLVQFLFKYQMKPEITKAEILSVIKNYEDHPFLPFSEASECMLLVFGI 189
Db 98 FRAVITKKVADLVGFLLLKYRAREPVTKAEMLSVKNYKHCFFEIFGKASESLQLVFGI 157
Qy 190 DVKEVDPGHSFVLVTSGLTYDGMLSDVQSMPTKGIILILSIIFIEGYCTPREVIEWA 249
Db 158 DVKEADPTGHSYVLVTCIGSYDGLGDNQIMPKTGFLIIVLVMIAMEGGHAPPEEIIWE 217
Qy 250 LNMGLYDGMHELIYGEPRKLLTQDWQENLYEVQVPGSDPARYEFLLWGPRAHAETRM 309
Db 218 LSVMEVDGHSAYGEPRKLLTQDLVQEKYLEYRQVDPDSDPARYEFLWGPRAALAEYSYV 277
Qy 310 SLKFLAKVNGSDPRSPPLWYERALKDEEE 339
Db 278 KLEVYIKVSARVRFPPSLREAAALREEE 307

RESULT 11
US-09-949-016-8559
; Sequence 8559, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
```

```
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8559
; LENGTH: 355
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8559

Query Match 42.7%; Score 807; DB 4; Length 355;
Best Local Similarity 53.6%; Pred. No. 9.6e-69;
Matches 177; Conservative 40; Mismatches 81; Indels 32; Gaps 4;

Qy 10 CMPEEDLOSQSETQGLEGAQAPLAVEEDASSSTSTSSFFSPSSSSSSSSSCYPLIPS 69
Db 56 CKPEALEAQOALGLVCQA-----ATSSSS-----PLVLG 87
Qy 70 TPEVSADDETPNPQSAQIACSPSVASLPDQSDGSSSOKESPSSTLQVLDPDSLSL 129
Db 88 TLEEVPTAGST-DPPQSPQASAFPTTINFRQPSGSSSREEGPSTSCIL---ESL 143
Qy 130 PRSEIDEKVTDLVQFLFKYQMKPEITKAEILSVIKNYEDHPFLPFSEASECMLLVFGI 189
Db 144 FRAVITKKVADLVGFLLLKYRAREPVTKAEMLSVKNYKHCFFEIFGKASESLQLVFGI 203
Qy 190 DVKEVDPGHSFVLVTSGLTYDGMLSDVQSMPTKGIILILSIIFIEGYCTPREVIEWA 249
Db 204 DVKEADPTGHSYVLVTCIGSYDGLGDNQIMPKTGFLIIVLVMIAMEGGHAPPEEIIWE 263
Qy 250 LNMGLYDGMHELIYGEPRKLLTQDWQENLYEVQVPGSDPARYEFLLWGPRAHAETRM 309
Db 264 LSVMEVDGHSAYGEPRKLLTQDLVQEKYLEYRQVDPDSDPARYEFLWGPRAALAEYSYV 323
Qy 310 SLKFLAKVNGSDPRSPPLWYERALKDEEE 339
Db 324 KLEVYIKVSARVRFPPSLREAAALREEE 353

RESULT 12
US-09-468-433C-22
; Sequence 22, Application US/09468433C
; Patent No. 6680191
; GENERAL INFORMATION:
; APPLICANT: LUCAS, Sophie; BOON-PALLEUR, Thierry
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES CODING FOR
; TUMOR REJECTION ANTIGEN PRECURSORS OF MEMBERS OF THE MAGE-C ANF
; TITLE OF INVENTION: MAGE-B FAMILIES AND USES THEREOF
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 801 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/468,433C
; FILING DATE: December 17, 1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/066,281
; FILING DATE: April 24, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/845,528
; FILING DATE: April 25, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mary Anne Schofield
; REGISTRATION NUMBER: 36,669
```

REFERENCE/DOCKET NUMBER: LUD 5611 JBL/MAS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 662-0200
TELEFAX: (202) 662-4643
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 346
TYPE: amino acid
STRANDEDNESS: single-stranded
TOPOLOGY: linear
US-09-468-433C-22

Query Match 41.9%; Score 793; DB 4; Length 346;
Best Local Similarity 49.9%; Pred. No. 2e-67;
Matches 175; Conservative 43; Mismatches 91; Indels 42; Gaps 6;
QY 1 MPRAPKRCMPREDLQSQSETQGLEGAQAAPLAVEDASSTSTSSFPSSSSSSSS 60
DB 1 MPLFPNLPRLSPEDFQNPSTEDLVAQDSIDEEEDASSTG-SSSFHFLFPSSSSLS 59
QY 61 SSCYPL--IPST-----PEEVSADDETPNPQSA 87
DB 60 SS--PLSPPLSTLILGVDEDMPAAGMPPLQSPPEIPQGPPLKISPGQPPQSP 117
QY 88 QIACSSPSVVASPLDOSDEGSSSQKEESPSTLQVLPDSESLPRSEIDEKVTDLVQLLF 147
DB 118 LDSCSSPLLWRL-----DEESSE-EDTATWHALPESESLPRYALDEKVAELVQLLL 171
QY 148 KYQKEPITKAILESIVKRYEDHFPPLPSEASECMLLVFGIDVKEVDPGHSFVLVTS 207
DB 172 KYQKEPITKAELTIVIKKYDYFPMIFGKAHEFTIELFGIALTDMDPNHSYFFEDTL 231
QY 208 GLTVDGMLSDVQSMPTGILILISIFIEGYCTPEEVIWEALNMGLYDGMELHYGE 267
DB 232 DLTYEGLIDQGMKPKNCLLILSMIFIKGSCVPEEVIWEVLSAIGVCAGREHYGDP 291
QY 268 RKLITQDVQENTLEYRVQVPGSDPARYEFYLGWGRAHAEIRKMSLLKFLAKV 318
DB 292 RKLITWQVKLEYREVNSAPPVRYEFLWGRAHSEAKSRSLRVFIQAI 342

RESULT 13
US-08-928-615-2
Sequence 2, Application US/08928615
Patent No. 5965535
GENERAL INFORMATION:
APPLICANT: Chau, Pascal
APPLICANT: Stroobant, Vincent
APPLICANT: Boon, Thierry
APPLICANT: van der Bruggen, Pierre
TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED
TITLE OF INVENTION: BY HLA CLASS II MOLECULES
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: MA
COUNTRY: U.S.A.
ZIP: 02210-2211
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,615
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Van Amsterdam, John R.
REGISTRATION NUMBER: 40,212
REFERENCE/DOCKET NUMBER: L0461/7017

TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 314 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-928-615-2

Query Match 41.4%; Score 783.5; DB 2; Length 314;
Best Local Similarity 48.5%; Pred. No. 1.4e-66;
Matches 165; Conservative 59; Mismatches 89; Indels 27; Gaps 5;
QY 1 MPRAPKRCMPREDLQSQSETQGLEGAQAAPLAVEDASSTSTSSFPSSSSSSSS 60
DB 1 MPLEQRSORCKPEEGLEARGEALGLVGAQAAPATEQEENASSST----- 44
QY 61 SSCYPLIPSTPEEVSADDETPNPQSAQIACSSPSVVASLPL-DQSDGSSSQKEESPST 119
DB 45 -----LVEVTLEVPA-AESPPDPQSPQASSLPTTM-NYPLWSQSYEDHPPLEFSEA 97
QY 120 LQVLPDSESLPRSEIDEKVTDLVQFLLFKYQMKPEITKAILESIVKRYEDHPPLEFSEA 179
DB 98 ---FPDLESEFQAALSRKVAELVHFLLLKYRAREPVTKAEMLGSVVGNWQYPPVIFSKA 154
QY 180 SECMLLVFGIDVKEVDPGHSFVLVTSGLTVDGMLSDVQSMPTGILILISIFIEGY 239
DB 155 SSSLQVLFVGIEMLEVDPIGHLYIFATCLGLSYDGLGDNQIMPKAGLLIVLAIAREGD 214
QY 240 CYPEEVIWEALNMGLYDGMELHYGEPRKLLTQDWMQENLYEYRQVPGSDPARYEFYLGW 299
DB 215 CAPEEKIWEELSLEVFEGRESILGDPKLLTQHFVQENLYEYRQVPGSDPARYEFYLGW 274
QY 300 PRAHAIRKMSLLKFLAKVNGSDPRSPFLWYBEALKDEEE 339
DB 275 PRALVETSYKVLHNMVKISGGPHISYPLHWHVLEEGEE 314

RESULT 14
US-09-166-448-2
Sequence 2, Application US/09166448
Patent No. 6291430
GENERAL INFORMATION:
APPLICANT: Chau, Pascal
APPLICANT: Vantomme, Valrie
APPLICANT: Stroobant, Vincent
APPLICANT: Boon-Falleur, Thierry
APPLICANT: van der Bruggen, Pierre
APPLICANT: Thielemans, Kris
APPLICANT: Cortbals, Jurgen
TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES
FILE REFERENCE: L0461/7052
CURRENT APPLICATION NUMBER: US/09/166,448
CURRENT FILING DATE: 1998-10-05
NUMBER OF SEQ ID NOS: 81
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 314
TYPE: PRT
ORGANISM: Homo sapiens
US-09-166-448-2
Query Match 41.4%; Score 783.5; DB 3; Length 314;
Best Local Similarity 48.5%; Pred. No. 1.4e-66;
Matches 165; Conservative 59; Mismatches 89; Indels 27; Gaps 5;
QY 1 MPRAPKRCMPREDLQSQSETQGLEGAQAAPLAVEDASSTSTSSFPSSSSSSSS 60
DB 1 MPLEQRSORCKPEEGLEARGEALGLVGAQAAPATEQEENASSST----- 44

Search completed: November 15, 2005, 15:45:52
Job time : 62.5476 secs

```
Qy 61 SSCYPLIPSTPEEVSADDETNPQSAQIACSSPSVVASLPL-DQSDEGSSSQKEESPST 119
Db 45 -----LVEVTIGEYPA-AESDPDPQSGASLPTTM-NYPLWSQSYEDSSNQEEGPST 97

Qy 120 LQVLPDSESLPRSIDEKVTDLVFLFKYQMKPEPTKAEILESIVKNEYDHPFLFSEA 179
Db 98 ---FPDLESEFQAALSRKVAELVHFLLLKYRAREPVTKAEMLGSVGVGNWQYFFVIFSKA 154

Qy 180 SECMLLVFGIDVKEVDPTGHSFVLVTSIGLTYDGMLSDVQSMPTGILILISIFIEGY 239
Db 155 SSSQLVFGIELMEVDPIGHLYIFATCLGLSYDGLGDNQIMPAGLLIIVLAIAREGD 214

Qy 240 CTPEEVIWEALNMGLYDGMELHYGEPRKLLTQDWQENLYEYRQVPGSDPARYEFLWG 299
Db 215 CAPEEKIWEELSLEVEFEGREDSILGDPKLLTQHFVQENLYEYRQVPGSDPARYEFLWG 274

Qy 300 PRAHAEIRKMSLLKFLAKVNGSDPRSPLWYEEALKDDEE 339
Db 275 PRALVETSYVKVLHMHVWKISGPHISYPLHFWVLRGEE 314

RESULT 15
US-09-348-933-2
; Sequence 2, Application US/09348933
; Patent No. 6369211
; GENERAL INFORMATION:
; APPLICANT: Chau, Pascal
; APPLICANT: Stroobant, Vincent
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: van der Bruggen, Pierre
; TITLE OF INVENTION: WAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES
; FILE REFERENCE: L0461/7065
; CURRENT APPLICATION NUMBER: US/09/348,933
; EARLIER APPLICATION NUMBER: US 08/928,615
; EARLIER FILING DATE: 1997-09-12
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-348-933-2

Query Match 41.4%; Score 783.5; DB 3; Length 314;
Best Local Similarity 48.5%; Pred. No. 1.4e-66;
Matches 165; Conservative 59; Mismatches 89; Indels 27; Gaps 5;

Qy 1 MPRAKQRQCMPEEDLQSQSETQGLEGAQAPLAVEEDASSSTSTSSFPSPSSSSSSSS 60
Db 1 MPLEQRQHQCKPERGLEARGEALGVGAQAPATEQEAAASSST----- 44

Qy 61 SSCYPLIPSTPEEVSADDETNPQSAQIACSSPSVVASLPL-DQSDEGSSSQKEESPST 119
Db 45 -----LVEVTIGEYPA-AESDPDPQSGASLPTTM-NYPLWSQSYEDSSNQEEGPST 97

Qy 120 LQVLPDSESLPRSIDEKVTDLVFLFKYQMKPEPTKAEILESIVKNEYDHPFLFSEA 179
Db 98 ---FPDLESEFQAALSRKVAELVHFLLLKYRAREPVTKAEMLGSVGVGNWQYFFVIFSKA 154

Qy 180 SECMLLVFGIDVKEVDPTGHSFVLVTSIGLTYDGMLSDVQSMPTGILILISIFIEGY 239
Db 155 SSSQLVFGIELMEVDPIGHLYIFATCLGLSYDGLGDNQIMPAGLLIIVLAIAREGD 214

Qy 240 CTPEEVIWEALNMGLYDGMELHYGEPRKLLTQDWQENLYEYRQVPGSDPARYEFLWG 299
Db 215 CAPEEKIWEELSLEVEFEGREDSILGDPKLLTQHFVQENLYEYRQVPGSDPARYEFLWG 274

Qy 300 PRAHAEIRKMSLLKFLAKVNGSDPRSPLWYEEALKDDEE 339
Db 275 PRALVETSYVKVLHMHVWKISGPHISYPLHFWVLRGEE 314
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 15, 2005, 15:35:58 ; Search time 219.643 Seconds
(without alignments)
702.928 Million cell updates/sec

Title: US-09-856-812b-1
Perfect score: 1891
Sequence: 1 MPRAPKRCQWPEEDLQSQS.....DTTAMASASSATGSEFSYPE 369

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1891	100.0	369	14	US-10-036-542-84
2	1891	100.0	369	15	US-10-188-832-149
3	1891	100.0	369	17	US-10-658-884-4
4	1891	100.0	369	18	US-10-756-149-4721
5	1852	97.9	383	14	US-10-029-386-32058
6	911	48.2	319	17	US-10-482-029-188
7	854	45.2	317	14	US-10-157-031-52
8	854	45.2	317	17	US-10-482-029-148
9	854	45.2	317	18	US-10-756-149-4740
10	849	44.9	317	15	US-10-218-095-2
11	846.5	44.8	315	14	US-10-093-766-40
					Sequence 84, Appl
					Sequence 149, Appl
					Sequence 4, Appl1
					Sequence 4721, Ap
					Sequence 32058, A
					Sequence 188, App
					Sequence 52, Appl
					Sequence 148, App
					Sequence 4740, Ap
					Sequence 2, Appl1
					Sequence 40, Appl

12	846.5	44.8	315	14	US-10-157-031-54	Sequence 54, Appl
13	846.5	44.8	315	15	US-10-295-027-366	Sequence 366, App
14	846.5	44.8	315	16	US-10-473-127-1079	Sequence 1079, Ap
15	846.5	44.8	315	16	US-10-473-127-1087	Sequence 1087, Ap
16	846.5	44.8	315	16	US-10-473-127-1091	Sequence 1091, Ap
17	846.5	44.8	315	16	US-10-473-127-1120	Sequence 1120, Ap
18	846.5	44.8	315	17	US-10-473-127-1122	Sequence 1122, Ap
19	846.5	44.8	315	17	US-10-482-029-168	Sequence 168, App
20	846.5	44.8	315	18	US-10-756-149-4729	Sequence 4729, Ap
21	840.5	44.4	315	16	US-10-473-127-1082	Sequence 1082, Ap
22	811.5	42.9	316	16	US-10-473-127-1085	Sequence 1085, Ap
23	809	42.8	1342	17	US-10-856-272-14	Sequence 14, Appl
24	807	42.7	308	17	US-10-729-830-9	Sequence 9, Appl1
25	807	42.7	309	9	US-09-766-889A-2	Sequence 2, Appl1
26	807	42.7	309	13	US-10-085-108-10	Sequence 10, Appl
27	807	42.7	309	14	US-10-160-237-10	Sequence 10, Appl
28	807	42.7	309	15	US-10-117-937-71	Sequence 71, Appl
29	807	42.7	309	15	US-10-296-734-828	Sequence 828, App
30	807	42.7	309	16	US-10-741-466-6	Sequence 6, Appl1
31	807	42.7	309	16	US-10-657-022-71	Sequence 71, Appl
32	807	42.7	309	17	US-10-866-484-6	Sequence 6, Appl1
33	807	42.7	309	17	US-10-482-029-92	Sequence 92, Appl
34	807	42.7	309	17	US-10-871-708-5	Sequence 5, Appl1
35	807	42.7	309	20	US-11-067-064-71	Sequence 71, Appl
36	807	42.7	309	20	US-11-067-159-71	Sequence 21, Appl
37	807	42.7	1052	14	US-10-856-272-21	Sequence 21, Appl
38	806	42.6	309	14	US-10-177-390-18	Sequence 18, Appl
39	800.5	42.3	314	15	US-10-117-937-72	Sequence 72, Appl
40	800.5	42.3	314	15	US-10-149-135-2439	Sequence 2439, Ap
41	800.5	42.3	314	16	US-10-657-022-72	Sequence 72, Appl
42	800.5	42.3	314	20	US-11-067-064-72	Sequence 72, Appl
43	800.5	42.3	314	20	US-11-067-159-72	Sequence 72, Appl
44	799	42.3	311	16	US-10-741-466-7	Sequence 7, Appl1
45	799	42.3	311	17	US-10-866-484-7	Sequence 7, Appl1

ALIGNMENTS

RESULT 1

US-10-036-542-84
; Sequence 84, Application US/10036542
; Publication No. US20030083481A1
; GENERAL INFORMATION:
; APPLICANT: Birsse et al.
; TITLE OF INVENTION: 25 Human Prostate and Prostate Cancer Associated Proteins
; FILE REFERENCE: PA002P1
; CURRENT APPLICATION NUMBER: US/10/036,542
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: PCT/US00/19666
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: 60/144,972
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: 60/148,681
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: 60/149,173
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/158,004
; PRIOR FILING DATE: 1999-10-06
; PRIOR APPLICATION NUMBER: 60/194,689
; PRIOR FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 157
; SOFTWARE: PatentIn Vpr. 2.0
; SEQ ID NO 84
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-036-542-84

Query Match 100.0%; Score 1891; DB 14; Length 369;
Best Local Similarity 100.0%; Pred. No. 3.1e-141;
Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRAPKRCMPEDLQSQSETQGLEGAQAPLAVEEDASSSTSTSSSPSPSPSSSSSS 60
Db 1 MPRAPKRCMPEDLQSQSETQGLEGAQAPLAVEEDASSSTSTSSSPSPSPSSSSSS 60
Qy 61 SSCYPLIPSTPEEVSADDETNPPOSAQIACSSPSVVASLPLDQSDGSSSQKESPSSTL 120
Db 61 SSCYPLIPSTPEEVSADDETNPPOSAQIACSSPSVVASLPLDQSDGSSSQKESPSSTL 120
Qy 121 QVLPDSSELSRSEIDEKVTDLVQFLFKYQMKPEITTKAEILLESVKNYEDHFPPLFSEAS 180
Db 121 QVLPDSSELSRSEIDEKVTDLVQFLFKYQMKPEITTKAEILLESVKNYEDHFPPLFSEAS 180
Qy 181 ECLMLVFGIDVKEVDPTGHSFVLVTSGLTYDGMLSDVQSMPTGILILILISIIIFIEGYC 240
Db 181 ECLMLVFGIDVKEVDPTGHSFVLVTSGLTYDGMLSDVQSMPTGILILILISIIIFIEGYC 240
Qy 241 TPEEVIWEALNMGLYDGMHELIYGEPRKLLTQDWQENYLEYRQVPGSDPARVEFLWGP 300
Db 241 TPEEVIWEALNMGLYDGMHELIYGEPRKLLTQDWQENYLEYRQVPGSDPARVEFLWGP 300
Qy 301 RAHAIEIRKMSLLKFLAKVNGSDPRSFPPLWYEALKDEBEERAQDRIATTTDDTTAMASASS 360
Db 301 RAHAIEIRKMSLLKFLAKVNGSDPRSFPPLWYEALKDEBEERAQDRIATTTDDTTAMASASS 360
Qy 361 ATGSFSYPE 369
Db 361 ATGSFSYPE 369

RESULT 2

US-10-188-832-149
; Sequence 149, Application US/10188832
; Publication No. US20040076955A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Bladder Cancer, Compositions
; TITLE OF INVENTION: and Methods of Screening for Modulators of Bladder
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 018501-002330US
; CURRENT APPLICATION NUMBER: US/10/188,832
; CURRENT FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: US 60/302,814
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: US 60/310,099
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/343,705
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/372,246
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 149
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-188-832-149

Query Match 100.0%; Score 1891; DB 15; Length 369;
Best Local Similarity 100.0%; Pred. No. 3.1e-141;
Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRAPKRCMPEDLQSQSETQGLEGAQAPLAVEEDASSSTSTSSSPSPSPSSSSSS 60
Db 1 MPRAPKRCMPEDLQSQSETQGLEGAQAPLAVEEDASSSTSTSSSPSPSPSSSSSS 60
Qy 61 SSCYPLIPSTPEEVSADDETNPPOSAQIACSSPSVVASLPLDQSDGSSSQKESPSSTL 120
Db 61 SSCYPLIPSTPEEVSADDETNPPOSAQIACSSPSVVASLPLDQSDGSSSQKESPSSTL 120

Qy 121 QVLPDSSELSRSEIDEKVTDLVQFLFKYQMKPEITTKAEILLESVKNYEDHFPPLFSEAS 180
Db 121 QVLPDSSELSRSEIDEKVTDLVQFLFKYQMKPEITTKAEILLESVKNYEDHFPPLFSEAS 180
Qy 181 ECLMLVFGIDVKEVDPTGHSFVLVTSGLTYDGMLSDVQSMPTGILILILISIIIFIEGYC 240
Db 181 ECLMLVFGIDVKEVDPTGHSFVLVTSGLTYDGMLSDVQSMPTGILILILISIIIFIEGYC 240
Qy 241 TPEEVIWEALNMGLYDGMHELIYGEPRKLLTQDWQENYLEYRQVPGSDPARVEFLWGP 300
Db 241 TPEEVIWEALNMGLYDGMHELIYGEPRKLLTQDWQENYLEYRQVPGSDPARVEFLWGP 300
Qy 301 RAHAIEIRKMSLLKFLAKVNGSDPRSFPPLWYEALKDEBEERAQDRIATTTDDTTAMASASS 360
Db 301 RAHAIEIRKMSLLKFLAKVNGSDPRSFPPLWYEALKDEBEERAQDRIATTTDDTTAMASASS 360
Qy 361 ATGSFSYPE 369
Db 361 ATGSFSYPE 369
RESULT 3
US-10-658-884-4
; Sequence 4, Application US/10658884
; Publication No. US20050019304A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL HUMAN MAGE-LIKE PROTEIN
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/658,884
; FILING DATE: 09-Sep-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/773,870
; FILING DATE: 27-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0179 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX: <unknown>
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 369 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 533511
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-658-884-4

Query Match 100.0%; Score 1891; DB 17; Length 369;
Best Local Similarity 100.0%; Pred. No. 3.1e-141;
Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy 1 MPRAPKRCRCMPEDLQSQSTQGLEGAQAPLAVEEDASSSTSTSSFPSSSSSSSS 60
Db 1 MPRAPKRCRCMPEDLQSQSTQGLEGAQAPLAVEEDASSSTSTSSFPSSSSSSSS 60
Qy 61 SSCYPLIPSTPEEVSADDETPNPQSAQIACSSPSVVASLPLDQSDGSSSQKEESPSTL 120
Db 61 SSCYPLIPSTPEEVSADDETPNPQSAQIACSSPSVVASLPLDQSDGSSSQKEESPSTL 120
Qy 121 QVLPDSSELPSEIDKVTDLVQFLFKYQMKPITKAEILSVIKNYEDHFPPLFSEAS 180
Db 121 QVLPDSSELPSEIDKVTDLVQFLFKYQMKPITKAEILSVIKNYEDHFPPLFSEAS 180
Qy 181 ECVLLVFGIDVKEVDPTGHSFVLVTSGLTYDGM LSVQSMPTKGIILILSIIFIEGYC 240
Db 181 ECVLLVFGIDVKEVDPTGHSFVLVTSGLTYDGM LSVQSMPTKGIILILSIIFIEGYC 240
Qy 241 TPEEVIWEALNMGLYDGMELIYGEPRKLLTQDWQENYLEYRQVPGSDPARYEFPLWGP 300
Db 241 TPEEVIWEALNMGLYDGMELIYGEPRKLLTQDWQENYLEYRQVPGSDPARYEFPLWGP 300
Qy 301 RAHAERKMSLLKFLAKVNGSDPRSPFLWYEEALKDEEERAQDRIATTTDDTTAMASASS 360
Db 301 RAHAERKMSLLKFLAKVNGSDPRSPFLWYEEALKDEEERAQDRIATTTDDTTAMASASS 360
Qy 361 ATGSFSYPE 369
Db 361 ATGSFSYPE 369
```

RESULT 4

```
US-10-756-149-4721
; Sequence 4721, Application US/10756149
; Publication No. US20050181375A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND
; TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
; FILE REFERENCE: file
; CURRENT APPLICATION NUMBER: US/10756.149
; CURRENT FILING DATE: 2004-01-12
; NUMBER OF SEQ ID NOS: 5818
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 4721
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-756-149-4721
```

```
Query Match 100.0%; Score 1891; DB 18; Length 369;
Best Local Similarity 100.0%; Pred. No. 3.1e-141;
Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRAPKRCRCMPEDLQSQSTQGLEGAQAPLAVEEDASSSTSTSSFPSSSSSSSS 60
Db 1 MPRAPKRCRCMPEDLQSQSTQGLEGAQAPLAVEEDASSSTSTSSFPSSSSSSSS 60
Qy 61 SSCYPLIPSTPEEVSADDETPNPQSAQIACSSPSVVASLPLDQSDGSSSQKEESPSTL 120
Db 61 SSCYPLIPSTPEEVSADDETPNPQSAQIACSSPSVVASLPLDQSDGSSSQKEESPSTL 120
Qy 121 QVLPDSSELPSEIDKVTDLVQFLFKYQMKPITKAEILSVIKNYEDHFPPLFSEAS 180
Db 121 QVLPDSSELPSEIDKVTDLVQFLFKYQMKPITKAEILSVIKNYEDHFPPLFSEAS 180
Qy 181 ECVLLVFGIDVKEVDPTGHSFVLVTSGLTYDGM LSVQSMPTKGIILILSIIFIEGYC 240
Db 181 ECVLLVFGIDVKEVDPTGHSFVLVTSGLTYDGM LSVQSMPTKGIILILSIIFIEGYC 240
Qy 241 TPEEVIWEALNMGLYDGMELIYGEPRKLLTQDWQENYLEYRQVPGSDPARYEFPLWGP 300
Db 241 TPEEVIWEALNMGLYDGMELIYGEPRKLLTQDWQENYLEYRQVPGSDPARYEFPLWGP 300
```

```
Qy 301 RAHAERKMSLLKFLAKVNGSDPRSPFLWYEEALKDEEERAQDRIATTTDDTTAMASASS 360
Db 301 RAHAERKMSLLKFLAKVNGSDPRSPFLWYEEALKDEEERAQDRIATTTDDTTAMASASS 360
Qy 361 ATGSFSYPE 369
Db 361 ATGSFSYPE 369

RESULT 5
US-10-029-386-32058
; Sequence 32058, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
; SEQ ID NO 32058
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AF134576.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.8
; OTHER INFORMATION: SWISSPROT HIT: P43363, EVALUE 0.00e+00
US-10-029-386-32058
```

```
Query Match 97.9%; Score 1852; DB 14; Length 383;
Best Local Similarity 100.0%; Pred. No. 4e-138;
Matches 362; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRAPKRCRCMPEDLQSQSTQGLEGAQAPLAVEEDASSSTSTSSFPSSSSSSSS 60
Db 22 MPRAPKRCRCMPEDLQSQSTQGLEGAQAPLAVEEDASSSTSTSSFPSSSSSSSS 81
Qy 61 SSCYPLIPSTPEEVSADDETPNPQSAQIACSSPSVVASLPLDQSDGSSSQKEESPSTL 120
Db 82 SSCYPLIPSTPEEVSADDETPNPQSAQIACSSPSVVASLPLDQSDGSSSQKEESPSTL 141
Qy 121 QVLPDSSELPSEIDKVTDLVQFLFKYQMKPITKAEILSVIKNYEDHFPPLFSEAS 180
Db 142 QVLPDSSELPSEIDKVTDLVQFLFKYQMKPITKAEILSVIKNYEDHFPPLFSEAS 201
Qy 181 ECVLLVFGIDVKEVDPTGHSFVLVTSGLTYDGM LSVQSMPTKGIILILSIIFIEGYC 240
Db 202 ECVLLVFGIDVKEVDPTGHSFVLVTSGLTYDGM LSVQSMPTKGIILILSIIFIEGYC 261
Qy 241 TPEEVIWEALNMGLYDGMELIYGEPRKLLTQDWQENYLEYRQVPGSDPARYEFPLWGP 300
Db 262 TPEEVIWEALNMGLYDGMELIYGEPRKLLTQDWQENYLEYRQVPGSDPARYEFPLWGP 321
Qy 301 RAHAERKMSLLKFLAKVNGSDPRSPFLWYEEALKDEEERAQDRIATTTDDTTAMASASS 360
Db 322 RAHAERKMSLLKFLAKVNGSDPRSPFLWYEEALKDEEERAQDRIATTTDDTTAMASASS 381
Qy 361 AT 362
Db 382 AT 383
```

```
RESULT 6
US-10-482-029-188
; Sequence 188, Application US/10482029
; Publication No. US20050037445A1
; GENERAL INFORMATION:
; APPLICANT: ODIN medical A/S
; TITLE OF INVENTION: Oncology drug innovation
; FILE REFERENCE: P 573 PC00
; CURRENT APPLICATION NUMBER: US/10/482,029
; CURRENT FILING DATE: 2003-12-29
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 188
; LENGTH: 319
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-482-029-188

Query Match      48.2%; Score 911; DB 17; Length 319;
Best Local Similarity 54.0%; Pred. No. 1.1e-63;
Matches 183; Conservative 53; Mismatches 81; Indels 22; Gaps 2;

Qy 1 MPRAPKRCRCMPEDLQSQSETQGLEGAQAAPLAVEEDASSSTSTSSFPSPSSSSSS 60
Db 1 MPEQRSQCHKPEEGLOQAEEDLGLVGAQAALQAEQEAAPFSSST----- 44

Qy 61 SSCYPLIPSTPEEVSADDETPNPQSAQIACSSPSVVASLPDQSDGSSSQKEESPSTL 120
Db 45 -----LNVGTLEELPA-AESAPSPQOEESFSTAMDAIFGSLSDGSGSQKEGPST 98

Qy 121 QVLPDSESLPRSEIDKVTDLVQFLFKYQMKPITKAEILSVIKNYEDHFPLLPSEAS 180
Db 99 PDLDIPESFSQDILHDKDIIVHLLLRKYRVKGLITKAEMLGSGVKNKEDTFPIFRAS 158

Qy 181 ECLMLVFGIDVKEVDPTGSHFVLVTSGLTYDGMQLSDVQSMPTKGLILILISIFIEGYC 240
Db 159 VCMQLLFGIDVKEVDPTGSHFVLVTSGLTYDGMQLSDVQSMPTKGLILILISIFIEGYC 218

Qy 241 TPEEVIWEALNMGLYDGMHEHLYGEPKRLLTQDWQENYLEYRQVPGSDPARYEFWLGP 300
Db 219 IPEEVMWEVLGIMGYAGREHFLFGEPRKRLLTQDWQENYLEYRQVPGSDPARYEFWLGP 278

Qy 301 RAHAERIKMSLLKFLAKVNGSDPRSFPPLWYEEALKDDEE 339
Db 279 RAHAETSKMKVLEYIANANGRDPTSYPSLYEDALREEGE 317

RESULT 7
US-10-157-031-52
; Sequence 52, Application US/10157031
; Publication No. US20030108890A1
; GENERAL INFORMATION:
; APPLICANT: Baranova, A. V.
; APPLICANT: Yankovsky, N. K.
; APPLICANT: Kozlov, A. P.
; APPLICANT: Lobashov, A. V.
; APPLICANT: Krukovskaya, L. L.
; TITLE OF INVENTION: In silico screening for phenotype-associated expressed sequences
; FILE REFERENCE: 2760-103
; CURRENT APPLICATION NUMBER: US/10/157,031
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 415
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-157-031-52

Query Match      45.2%; Score 854; DB 14; Length 317;
Best Local Similarity 51.9%; Pred. No. 3.7e-59;
Matches 176; Conservative 51; Mismatches 88; Indels 24; Gaps 3;

Qy 1 MPRAPKRCRCMPEDLQSQSETQGLEGAQAAPLAVEEDASSSTSTSSFPSPSSSSSS 60
Db 1 MSSEQKSQCHKPEEGVEAQEALGLVGAQAAPTEEQEAIVSSSS----- 44

Qy 61 SSCYPLIPSTPEEVSADDETPNPQSAQIACSSPSVVASLPDQSDGSSSQKEESPSTL 120
Db 45 -----PLVPGTLEEVPA-AESAGPPQSPQASALPTTISFTCWRQPNEGSSQKEEGPST- 98

Qy 121 QVLPDSESLPRSEIDKVTDLVQFLFKYQMKPITKAEILSVIKNYEDHFPLLPSEAS 180
Db 99 --SPDAESLFRALSNNKVDLAHFLKRYRAKELVTKAEMLERVIKRYKCFPVIFGKAS 156

Qy 181 ECLMLVFGIDVKEVDPTGSHFVLVTSGLTYDGMQLSDVQSMPTKGLILILISIFIEGYC 240
Db 157 ESKMIFGIDVKEVDPTGSHFVLVTSGLTYDGMQLSDVQSMPTKGLILILISIFIEGYC 216

Qy 241 TPEEVIWEALNMGLYDGMHEHLYGEPKRLLTQDWQENYLEYRQVPGSDPARYEFWLGP 300
Db 217 ASEEEIWEELGVMGVYDGRHTVYGEPRKRLLTQDWQENYLEYRQVPGSDPARYEFWLGP 276

Qy 301 RAHAERIKMSLLKFLAKVNGSDPRSFPPLWYEEALKDDEE 339
Db 277 RALAETSIVKLVHVRVNRVARIAYPSLREAAALLEEE 315

RESULT 8
US-10-482-029-148
; Sequence 148, Application US/10482029
; Publication No. US20050037445A1
; GENERAL INFORMATION:
; APPLICANT: ODIN medical A/S
; TITLE OF INVENTION: Oncology drug innovation
; FILE REFERENCE: P 573 PC00
; CURRENT APPLICATION NUMBER: US/10/482,029
; CURRENT FILING DATE: 2003-12-29
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 148
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-482-029-148

Query Match      45.2%; Score 854; DB 17; Length 317;
Best Local Similarity 51.9%; Pred. No. 3.7e-59;
Matches 176; Conservative 51; Mismatches 88; Indels 24; Gaps 3;

Qy 1 MPRAPKRCRCMPEDLQSQSETQGLEGAQAAPLAVEEDASSSTSTSSFPSPSSSSSS 60
Db 1 MSSEQKSQCHKPEEGVEAQEALGLVGAQAAPTEEQEAIVSSSS----- 44

Qy 61 SSCYPLIPSTPEEVSADDETPNPQSAQIACSSPSVVASLPDQSDGSSSQKEESPSTL 120
Db 45 -----PLVPGTLEEVPA-AESAGPPQSPQASALPTTISFTCWRQPNEGSSQKEEGPST- 98

Qy 121 QVLPDSESLPRSEIDKVTDLVQFLFKYQMKPITKAEILSVIKNYEDHFPLLPSEAS 180
Db 99 --SPDAESLFRALSNNKVDLAHFLKRYRAKELVTKAEMLERVIKRYKCFPVIFGKAS 156

Qy 181 ECLMLVFGIDVKEVDPTGSHFVLVTSGLTYDGMQLSDVQSMPTKGLILILISIFIEGYC 240
Db 157 ESKMIFGIDVKEVDPTGSHFVLVTSGLTYDGMQLSDVQSMPTKGLILILISIFIEGYC 216

Qy 241 TPEEVIWEALNMGLYDGMHEHLYGEPKRLLTQDWQENYLEYRQVPGSDPARYEFWLGP 300
Db 217 ASEEEIWEELGVMGVYDGRHTVYGEPRKRLLTQDWQENYLEYRQVPGSDPARYEFWLGP 276

Qy 301 RAHAERIKMSLLKFLAKVNGSDPRSFPPLWYEEALKDDEE 339
Db 277 RALAETSIVKLVHVRVNRVARIAYPSLREAAALLEEE 315

RESULT 9
US-10-157-031-52
; Sequence 52, Application US/10157031
; Publication No. US20030108890A1
; GENERAL INFORMATION:
; APPLICANT: Baranova, A. V.
; APPLICANT: Yankovsky, N. K.
; APPLICANT: Kozlov, A. P.
; APPLICANT: Lobashov, A. V.
; APPLICANT: Krukovskaya, L. L.
; TITLE OF INVENTION: In silico screening for phenotype-associated expressed sequences
; FILE REFERENCE: 2760-103
; CURRENT APPLICATION NUMBER: US/10/157,031
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 415
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-157-031-52

Query Match      45.2%; Score 854; DB 14; Length 317;
Best Local Similarity 51.9%; Pred. No. 3.7e-59;
Matches 176; Conservative 51; Mismatches 88; Indels 24; Gaps 3;
```



```

US-10-756-149-4740
; Sequence 4740, Application US/10756149
; Publication No. US20050181375A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND
; FILE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
; FILE REFERENCE: file
; CURRENT APPLICATION NUMBER: US/10/756.149
; CURRENT FILING DATE: 2004-01-12
; NUMBER OF SEQ ID NOS: 5818
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4740
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-756-149-4740

Query Match 45.2%; Score 854; DB 18; Length 317;
Best Local Similarity 51.9%; Pred. No. 3.7e-59;
Matches 176; Conservative 51; Mismatches 88; Indels 24; Gaps 3;

QY 1 MPRAPKRCMPEDLQSQSETQGLEGAQAAPLAVEEDASSSTSTSSFFSPSSSSSS 60
DB 1 MSSEQSKQCHCKPBEVGEAEALGLVGAQAPTTTEQEAASVSSS----- 44
QY 61 SSCYPLIPSTPEVSADDETNPQSAQIACSSPSVVASLPDQSDRGSSSQKEESPSTL 120
DB 45 ----PLVPGTLEEVPA-AESAGPPSPQASALPTTISFTCWQPNQEGSSSQEEGPST- 98
QY 121 QVLPDSLSRSEIDEKVTDLVQFLFKYQMKPEITKAEILSVIKNYEDHFFLLFSEAS 180
DB 99 --SPDAESLFREALSNKVDLAHLAKRYAKELVTKAEMLEKRVKNCFCFPVIFGKAS 156
QY 181 ECKMLVFGIDVKEVDPTGHSFVLVTSGLTYDGMUSDVQSMPTKGLILILSIIFIEGYC 240
DB 157 ESLKMFIDGIDVKEVDPTGHSFVLVTSGLTYDGMUSDVQSMPTKGLILILSIIFIEGYC 216
QY 241 TPERVWEALNMGLYDGMHELIYGEPRKLLTQDWQENYLEYRQVPGSDPARVEFLWGP 300
DB 217 ASEEEIWEELGVMGVYDGREHTVYGEPRKLLTQDWQENYLEYRQVPGSDPARVEFLWGP 276
QY 301 RAHAIRKMSLLKFLAKVNGSDPRSPFLWYEEALKDEEE 339
DB 277 RALAETSYVKVLEHVVRNARVRIAYPSLREAALEEE 315

RESULT 11
US-10-093-766-40
; Sequence 40, Application US/10093766
; Publication No. US20030013099A1
; GENERAL INFORMATION:
; APPLICANT: Laeak, Amy W.
; APPLICANT: Jones, David A.
; APPLICANT: Karpf, Adam R.
; TITLE OF INVENTION: GENES REGULATED BY DNA METHYLATION IN COLON TUMORS
; FILE REFERENCE: PA-0047 US
; CURRENT APPLICATION NUMBER: US/10/093.766
; CURRENT FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PERL Program
; SEQ ID NO 40
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030013099A1 2502336CD1
US-10-093-766-40

Query Match 44.8%; Score 846.5; DB 14; Length 315;
Best Local Similarity 51.0%; Pred. No. 1.4e-58;
Matches 172; Conservative 48; Mismatches 88; Indels 29; Gaps 3;

QY 3 RAPRQRCMPEDLQSQSETQGLEGAQAAPLAVEEDASSSTSTSSFFSPSSSSSSSS 62
DB 6 RSP----HCKPDEDLQAQEDLGLMGAQEPTEGEEETTSSD----- 43
QY 63 CYPLIPSTPEVSADDETNPQSAQIACSSPSVVASLPDQSDRGSSSQKEESPSTLQV 122
DB 44 -----SKEEVSAAGSS-SPPOSGGASSSISVYTTWQSDGSSSQKEESPSSVD 96
QY 123 LPDSLSRSEIDEKVTDLVQFLFKYQMKPEITKAEILSVIKNYEDHFFLLFSEASEC 182
DB 97 PAQLFEMFQEAALKVAELVHLLHKYRKEPVTKAEMLEKRVKNCFCFPVIFGKASEF 156
QY 183 MLLVFGIDVKEVDPTGHSFVLVTSGLTYDGMUSDVQSMPTKGLILILSIIFIEGYCTP 242
DB 157 MQVIFGTDVKEVDPTGHSFVLVTSGLTYDGMUSDVQSMPTKGLILILSIIFIEGYCTP 216
QY 243 BEVWEALNMGLYDGMHELIYGEPRKLLTQDWQENYLEYRQVPGSDPARVEFLWGP 302
DB 217 BEVWEALNMGLYDGMHELIYGEPRKLLTQDWQENYLEYRQVPGSDPARVEFLWGP 276

```

```

US-10-756-149-4740
; Sequence 4740, Application US/10756149
; Publication No. US20050181375A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND
; FILE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
; FILE REFERENCE: file
; CURRENT APPLICATION NUMBER: US/10/756.149
; CURRENT FILING DATE: 2004-01-12
; NUMBER OF SEQ ID NOS: 5818
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4740
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-756-149-4740

Query Match 45.2%; Score 854; DB 18; Length 317;
Best Local Similarity 51.9%; Pred. No. 3.7e-59;
Matches 176; Conservative 51; Mismatches 88; Indels 24; Gaps 3;

QY 1 MPRAPKRCMPEDLQSQSETQGLEGAQAAPLAVEEDASSSTSTSSFFSPSSSSSS 60
DB 1 MSSEQSKQCHCKPBEVGEAEALGLVGAQAPTTTEQEAASVSSS----- 44
QY 61 SSCYPLIPSTPEVSADDETNPQSAQIACSSPSVVASLPDQSDRGSSSQKEESPSTL 120
DB 45 ----PLVPGTLEEVPA-AESAGPPSPQASALPTTISFTCWQPNQEGSSSQEEGPST- 98
QY 121 QVLPDSLSRSEIDEKVTDLVQFLFKYQMKPEITKAEILSVIKNYEDHFFLLFSEAS 180
DB 99 --SPDAESLFREALSNKVDLAHLAKRYAKELVTKAEMLEKRVKNCFCFPVIFGKAS 156
QY 181 ECKMLVFGIDVKEVDPTGHSFVLVTSGLTYDGMUSDVQSMPTKGLILILSIIFIEGYC 240
DB 157 ESLKMFIDGIDVKEVDPTGHSFVLVTSGLTYDGMUSDVQSMPTKGLILILSIIFIEGYC 216
QY 241 TPERVWEALNMGLYDGMHELIYGEPRKLLTQDWQENYLEYRQVPGSDPARVEFLWGP 300
DB 217 ASEEEIWEELGVMGVYDGREHTVYGEPRKLLTQDWQENYLEYRQVPGSDPARVEFLWGP 276
QY 301 RAHAIRKMSLLKFLAKVNGSDPRSPFLWYEEALKDEEE 339
DB 277 RALAETSYVKVLEHVVRNARVRIAYPSLREAALEEE 315

RESULT 11
US-10-093-766-40
; Sequence 40, Application US/10093766
; Publication No. US20030013099A1
; GENERAL INFORMATION:
; APPLICANT: Laeak, Amy W.
; APPLICANT: Jones, David A.
; APPLICANT: Karpf, Adam R.
; TITLE OF INVENTION: GENES REGULATED BY DNA METHYLATION IN COLON TUMORS
; FILE REFERENCE: PA-0047 US
; CURRENT APPLICATION NUMBER: US/10/093.766
; CURRENT FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PERL Program
; SEQ ID NO 40
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030013099A1 2502336CD1
US-10-093-766-40

Query Match 44.8%; Score 846.5; DB 14; Length 315;
Best Local Similarity 51.0%; Pred. No. 1.4e-58;
Matches 172; Conservative 48; Mismatches 88; Indels 29; Gaps 3;

QY 3 RAPRQRCMPEDLQSQSETQGLEGAQAAPLAVEEDASSSTSTSSFFSPSSSSSSSS 62
DB 6 RSP----HCKPDEDLQAQEDLGLMGAQEPTEGEEETTSSD----- 43
QY 63 CYPLIPSTPEVSADDETNPQSAQIACSSPSVVASLPDQSDRGSSSQKEESPSTLQV 122
DB 44 -----SKEEVSAAGSS-SPPOSGGASSSISVYTTWQSDGSSSQKEESPSSVD 96
QY 123 LPDSLSRSEIDEKVTDLVQFLFKYQMKPEITKAEILSVIKNYEDHFFLLFSEASEC 182
DB 97 PAQLFEMFQEAALKVAELVHLLHKYRKEPVTKAEMLEKRVKNCFCFPVIFGKASEF 156
QY 183 MLLVFGIDVKEVDPTGHSFVLVTSGLTYDGMUSDVQSMPTKGLILILSIIFIEGYCTP 242
DB 157 MQVIFGTDVKEVDPTGHSFVLVTSGLTYDGMUSDVQSMPTKGLILILSIIFIEGYCTP 216
QY 243 BEVWEALNMGLYDGMHELIYGEPRKLLTQDWQENYLEYRQVPGSDPARVEFLWGP 302
DB 217 BEVWEALNMGLYDGMHELIYGEPRKLLTQDWQENYLEYRQVPGSDPARVEFLWGP 276

```


THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 15, 2005, 15:28:51 ; Search time 5.69048 Seconds
(without alignments)
611.696 Million cell updates/sec

Title: US-09-856-812B-42
Perfect score: 51
Sequence: 1 GLYDGMHL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	9	3	AAY71487 Human MAG
2	51	100.0	9	4	AAB31323 Exemplary
3	51	100.0	9	5	AAO17088 Human mag
4	51	100.0	9	6	ABJ19876 MHC bindi
5	51	100.0	9	8	ADG89586 Class I H
6	51	100.0	9	8	ADI19869 Human HLA
7	51	100.0	9	8	ADI19026 Human HLA
8	51	100.0	9	8	ADJ58374 Peptide p
9	51	100.0	9	8	ADL26560 Melanoma
10	51	100.0	9	8	ADR69760 Novel hyb
11	51	100.0	10	3	AAY71489 Human MAG
12	51	100.0	20	8	ADR69766 Novel hyb
13	51	100.0	369	3	AAY71485 Human MAG
14	51	100.0	369	6	ABR48215 Human pro
15	51	100.0	369	6	ABR48215 Human bla
16	51	100.0	369	6	ABU56516 Lung canc
17	51	100.0	383	8	ABO58424 Human gen
18	43	84.3	347	6	ADA55634 Human pro
19	41	80.4	9	3	AAY71488 Human MAG
20	41	80.4	10	3	AAY71490 Human MAG
21	41	80.4	318	3	ABR08734 Amino aci
22	41	80.4	318	8	ABR82457 Tumour-as
23	40	78.4	398	2	AAW24252 Ammonifex
24	40	78.4	398	6	ABU57355 A. degens
25	40	78.4	419	8	ADN20266 Bacterial

ALIGNMENTS

RESULT 1

AAAY71487
ID AAY71487 standard; peptide; 9 AA.
AC AAY71487;
XX
DT 12-OCT-2000 (first entry)
XX
DE Human MAGE-A10 nonapeptide-1.
XX
KW MAGE-A10; human; Tumour Rejection Antigen; TRA; Human Leucocyte Antigen; HLA; Major Histocompatibility Complex; MHC; cytolytic T-lymphocyte; CTL; immune response stimulator; prophylaxis; therapy; diagnosis; tumour; cancer; TNF; tumour necrosis factor; vaccine; cytostatic.
XX Homo sapiens.
OS
FN WO200032769-A2.
XX
PD 08-JUN-2000.
XX
PF 26-NOV-1999; 99WO-IB002018.
XX
PR 27-NOV-1998; 98GB-00026143.
XX (LUDW-) LUDWIG INST CANCER RES.
XX
PI Huang L, Van Pel A, Brasseur F, De Plaen E, Boon T, WPI; 2000-412317/35.
XX
PT Novel polypeptides expressed in tumor cells useful for treating cancers have an ability to complex with a major histocompatibility complex molecule and comprises a specific unbroken amino acid sequence.
XX
PT Claim 8; Page 36; 80pp; English.
XX
CC The patent discloses MAGE-A10 and MAGE-A8 polypeptide, nonapeptide and decapeptide sequences, that function as tumour rejection antigens (TRAAs). These peptides are capable of forming a complex with major histocompatibility complex (MHC) molecule type HLA-A2.1 (Human Leucocyte Antigen), that are recognised by T-lymphocytes and elicit an immune response from cytolytic T-lymphocytes (CTL). They function as an immune response stimulator. Tumour rejection antigens are useful in prophylaxis, therapy and diagnosis of tumours and are effective in controlling or preventing tumour growth. The present peptide sequence is the human MAGE-A10 nonapeptide-1, that corresponds to residues 254-262 of the MAGE-A10 protein. This peptide can serve as a tumour rejection antigen (TRA) and

CC in combination with adjuvants, can produce vaccines useful for treating a
 CC variety of tumours that express MAGE-A10

SQ Sequence 9 AA;

Query Match 100.0%; Score 51; DB 3; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLYDGMHGL 9
 |||||
 Db 1 GLYDGMHGL 9

RESULT 2

AAB31323
 ID AAB31323 standard; peptide; 9 AA.

XX AC AAB31323;

DT 20-APR-2001 (first entry)

XX Exemplary antigen characteristic of tumours and derived from MAGE-A10.

DE MAGE-A1; HLA; human leukocyte antigen; CD4+ T lymphocyte; cancer;

KW MAGE-A1 HLA class II-binding protein; vaccine.

XX OS Homo sapiens.

XX WO200078806-A1.

XX PD 28-DEC-2000.

XX PF 14-JUN-2000; 2000WO-US016287.

XX PR 18-JUN-1999; 99US-00336091.

XX PA (LUDW-) LUDWIG INST CANCER RES.

XX PI Van Snick J, Leche B, Chaux P, Boon-Falleur T, Van Der Bruggen P;

XX WPI; 2001-102698/11.

XX Novel MAGE-A1 human leukocyte antigen class II peptides which bind to and
 PT are presented to the class II molecules, useful for inducing immune
 PT response and treating cancers characterized by expression of MAGE-A1.
 XX Disclosure; Page 32; 78pp; English.

XX AAB31302-59 represent exemplary antigens which are characteristic of
 CC tumours. They can be used to enhance the immune response of vaccines
 CC comprising peptides derived from human MAGE-A1 HLA (human leukocyte
 CC antigen) class II-binding protein. Peptides derived from the MAGE-A1 HLA
 CC binding protein stimulate the activity and proliferation of CD4+ T
 CC lymphocytes. The MAGE-A1 HLA binding protein is useful as a diagnostic
 CC agent for diagnosing a disorder characterized by expression of MAGE-A1.
 CC The protein is used for treating a disorder characterized by expression
 CC of MAGE-A1 such as cancers e.g. melanoma, squamous cell carcinomas,
 CC colorectal carcinomas, osteosarcomas, and lymphocytic leukemias. Peptides
 CC derived from the MAGE-A1 HLA binding protein are useful in the production
 CC of anti-tumour vaccines

SQ Sequence 9 AA;

Query Match 100.0%; Score 51; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLYDGMHGL 9
 |||||
 Db 1 GLYDGMHGL 9

RESULT 3

AAO17088
 ID AAO17088 standard; peptide; 9 AA.

XX AC AAO17088;

DT 06-JUN-2002 (first entry)

XX Human mage-A10 protein antigen SEQ ID NO: 8.

XX Cryopreserved mature dendritic cell; antigen; vaccine; cytostatic;
 KW virucide; cancer; hepatitis B virus.

XX OS Homo sapiens.

XX WO200216560-A1.

XX PD 28-FEB-2002.

XX PF 24-AUG-2001; 2001WO-EP009790.

XX PR 24-AUG-2000; 2000DE-01041515.

XX PA (SCHU/) SCHULER G.

XX PI Schuler G, Schuler-Thurner B;

XX WPI; 2002-292062/33.

XX Preparation of cryopreserved, mature dendritic cells, useful in vaccines,
 PT comprises culturing immature cells on medium containing cocktail of
 PT maturation factors, then freezing.
 XX Disclosure; Fig 28; 87pp; German.

XX The present invention relates to a method for the preparation of ready-
 CC for-use, cryopreserved, mature dendritic cells comprising growing
 CC immature dendritic cells in a culture medium that includes a 'maturation
 CC cocktail' of one or more maturation stimuli and freezing the resulting
 CC matured cells in a freezing medium that does not contain heterologous
 CC serum. When loaded with antigens, the dendritic cells can be used as
 CC vaccines, e.g. against tumours and hepatitis B virus. The present
 CC sequence is an antigen described in the invention

SQ Sequence 9 AA;

Query Match 100.0%; Score 51; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLYDGMHGL 9
 |||||
 Db 1 GLYDGMHGL 9

RESULT 4

ABJ19876
 ID ABJ19876 standard; peptide; 9 AA.

XX AC ABJ19876;

DT 10-APR-2003 (first entry)

XX MHC binding peptide SEQ ID No 39.

XX Antirheumatic; antiallergic; antiarthritic; nootropic; neuroprotective;
 KW antiinflammatory; major histocompatibility complex; MHC;
 KW autoimmune disease; T cell; B cell; allergic disease; multiple sclerosis;
 KW rheumatoid arthritis; neurodegenerative disorder; Alzheimer's disease;
 KW inflammation; gene therapy; MHC binding peptide.

XX OS Synthetic.

PN WO200294981-A2.
 XX 28-NOV-2002.
 XX 16-MAY-2002; 2002WO-IL000383.
 XX 16-MAY-2001; 2001US-0290958P.
 PR 29-MAY-2001; 2001US-00865548.
 XX (TECR) TECHNION RES & DEV FOUND LTD.
 XX Barnea E, Beer I, Ziv T, Admon A, Dassau L, Buchsbaum S;
 XX WPI; 2003-210043/20.
 XX Identifying peptides that are capable of binding to major
 PT histocompatibility complex (MHC) molecules of a particular haplotype by
 PT analyzing peptides bound to the soluble and secreted form of the MHC
 PT molecules of the particular haplotype.
 XX Example; Fig 5D; 238pp; English.
 XX The invention relates to a novel method for identifying peptides
 CC originating from a particular cell type, which are capable of binding to
 CC major histocompatibility complex (MHC) molecules of a particular
 CC haplotype. The method comprises analysing peptides bound to the soluble
 CC and secreted form of the MHC molecules of the particular haplotype. The
 CC method is useful for identifying peptides for treating an autoimmune
 CC disease, such as T or B cell and/or allergic disease or condition,
 CC rheumatoid arthritis, or multiple sclerosis, neurodegenerative disorders,
 CC e.g. Alzheimer's disease, or diseases associated with inflammation. The
 CC sequences of the invention may be used in a gene therapy application.
 CC This sequence represents a peptide relating to the method for identifying
 CC MHC binding peptides of the invention
 XX
 XX Sequence 9 AA;
 Query Match 100.0%; Score 51; DB 6; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GLYDGMHEHL 9
 Db 1 GLYDGMHEHL 9
 RESULT 5
 ADG89586
 ID ADG89586 standard; peptide; 9 AA.
 AC ADG89586;
 XX 11-MAR-2004 (first entry)
 DE Class I HLA-restricted testis cancer antigen #21.
 XX metastatic cancer cell differentiation; mutated fibronectin;
 KW metastatic cancer; class I HLA-restricted; testis; cancer antigen.
 XX Unidentified.
 OS
 XX WO2003100027-A2.
 PN 04-DEC-2003.
 PD 28-MAY-2003; 2003WO-US016736.
 XX 28-MAY-2002; 2002US-0383530P.
 PR (BAYU) BAYLOR COLLEGE MEDICINE.
 XX Wang R;
 XX

DR WPI; 2004-035134/03.
 XX Identifying a cell that differentiates into a metastatic cancer cell,
 PT useful for preventing metastatic cancer, comprises identifying a mutated
 PT fibronectin in the cell.
 XX Disclosure; SEQ ID NO 29; 137pp; English.
 XX The invention comprises a method for identifying a cell that will
 CC differentiate into a metastatic cancer cell, the method involves
 CC identifying a mutated fibronectin in the cell. The method of the
 CC invention is useful for preventing metastatic cancer. The present amino
 CC acid sequence represents a Class I HLA-restricted testis cancer antigen.
 XX Sequence 9 AA;
 Query Match 100.0%; Score 51; DB 8; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GLYDGMHEHL 9
 Db 1 GLYDGMHEHL 9
 RESULT 6
 ADI19869
 ID ADI19869 standard; peptide; 9 AA.
 AC ADI19869;
 XX 22-APR-2004 (first entry)
 DT Human HLA-B*8 binding MAGE-3 peptide #11.
 DE HLA; human leucocyte antigen; melanoma; lung cancer; head cancer;
 XX neck cancer; MAGE-3; human.
 KW Homo sapiens.
 OS US2003228325-A1.
 PN 11-DEC-2003.
 PD 05-JUN-2002; 2002US-00164078.
 PF 05-JUN-2002; 2002US-00164078.
 PR (BILS/) BILSBOROUGH J.
 XX (SCHU/) SCHULTZ E.
 PA (PANI/) PANICHELLI C.
 PA (BOON/) BOON-FALLEUR T.
 PA (BRUG/) BRUGEN P V D.
 XX Blisborough J, Schultz E, Panichelli C, Boon-Falleur T;
 PI Bruggen PVD;
 PI WPI; 2004-042211/04.
 DR Treating subject with pathological condition having human leucocyte
 XX antigen-B18 molecules presented on cell surface by administering peptides
 XX to subject for generating immunologically active response against cells.
 PS Claim 22; SEQ ID NO 12; 15pp; English.
 XX The present invention relates to a peptide which binds HLA (human
 CC leucocyte antigen)-B18 to form T-cell epitope. The invention is useful
 CC for treating a pathological conditions such as melanoma, lung cancer and
 CC head and neck cancer. The present sequence is human HLA-B*8 binding MAGE-
 CC 3 peptide.
 XX Sequence 9 AA;
 SQ

```
Query Match      100.0%; Score 51; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLYDGMHHL 9
Db 1 GLYDGMHHL 9

RESULT 7
ADI19026
ID ADI19026 standard; peptide; 9 AA.
AC ADI19026;
DT 22-APR-2004 (first entry)
DE Human HLA-Cw6 binding MAGE-1 peptide #11.
KW MHC; major histocompatibility; therapy; cancer; melanoma; HLA-Cw6; human;
KW MAGE-1; cytostatic.
XX Homo sapiens.
OS US2003228308-A1.
XX PN
XX PD 11-DEC-2003.
XX PF 05-JUN-2002; 2002US-00164121.
XX PR 05-JUN-2002; 2002US-00164121.
XX PA (ZHAN/) ZHANG Y.
XX PA (TRAV/) TRAVERSARI C.
XX PA (BOON/) BOON-FALLEUR T.
XX PA (BRUG/) BRUGGEN P V D.
PI Zhang Y, Traversari C, Boon-Falleur T, Bruggen PVD;
XX WPI; 2004-042210/04.
DR
XX Treating subject with pathological condition having human leukocyte
PT antigen-Cw6 molecules presented on cell surface by administering peptides
PT to subject for generating immunologically active response against cells.
XX Example 7; SEQ ID NO 13; 15pp; English.
XX The present invention relates to peptides which form immunologically
CC active complexes with MHC molecules. The invention is useful for treating
CC a subject with pathological condition such as cancer which is melanoma by
CC presenting HLA-Cw6 molecules on the cell surface. The present sequence is
CC human HLA-Cw6 binding MAGE-1 peptide.
XX Sequence 9 AA;

Query Match      100.0%; Score 51; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLYDGMHHL 9
Db 1 GLYDGMHHL 9

RESULT 8
ADJ58374
ID ADJ58374 standard; peptide; 9 AA.
AC ADJ58374;
XX DT 06-MAY-2004 (first entry)
XX DE Peptide predicted to bind to HLA-A2 #34.

Query Match      100.0%; Score 51; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLYDGMHHL 9
Db 1 GLYDGMHHL 9

RESULT 9
ADL26560
ID ADL26560 standard; peptide; 9 AA.
XX AC ADL26560;
XX DT 03-JUN-2004 (first entry)
XX DE Melanoma cell line MAGE gene encoded HLA-A2 peptide.
XX cytostatic; gene therapy; vaccine; cancer; immune response.
XX Homo sapiens.
XX WO2004019886-A2.
XX PD 11-MAR-2004.
XX PF 29-AUG-2003; 2003WO-US027125.
XX PR 29-AUG-2002; 2002US-0407492P.
XX PA (CYTO-) CYTOCURE LLC.
XX
```

XX major histocompatibility complex; MHC; cytolytic T-cell; HLA-A2;
KW Cytostatic; cancer.
XX Synthetic.
OS
XX WO2004011483-A2.
XX PD 05-FEB-2004.
XX 23-JUL-2003; 2003WO-US023306.
XX 31-JUL-2002; 2002US-0400076P.
XX (LUDW-) LUDWIG INST CANCER RES.
XX PA (TORR-) TORREY PINES INST MOLECULAR STUDIES.
XX PI Valmori D, Ayyoub M, Pinilla C;
XX WPI; 2004-143815/14.
XX New isolated SSX-2 and SSX-2-related peptides that bind to human
PT leukocyte antigen (HLA) molecules, useful for diagnosing or treating
PT cancer, particularly melanoma.
XX Example 8; SEQ ID NO 34; 20pp; English.
XX The present invention relates to an isolated peptide which binds to a
CC major histocompatibility complex (MHC) molecule to form a complex that is
CC recognized by a cytolytic T-cell which recognizes and lyses cells
CC presenting complexes of HLA-A2 molecules comprising a sequence of 9 amino
CC acids fully defined in the specification, with the proviso that the
CC peptide is not the peptide of S17 itself. Specifically claimed is an HLA-
CC binding peptide comprising a sequence of 9 amino acids fully defined in
CC the specification. The composition and methods are useful for diagnosing
CC or treating cancer, particularly melanoma. The present sequence
CC represents a peptide predicted to bind to HLA-A2.
XX Sequence 9 AA;
SQ

Query Match 100.0%; Score 51; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GLYDGMHHL 9
Db 1 GLYDGMHHL 9

RESULT 9
ADL26560
ID ADL26560 standard; peptide; 9 AA.
XX AC ADL26560;
XX DT 03-JUN-2004 (first entry)
XX DE Melanoma cell line MAGE gene encoded HLA-A2 peptide.
XX cytostatic; gene therapy; vaccine; cancer; immune response.
XX Homo sapiens.
XX WO2004019886-A2.
XX PD 11-MAR-2004.
XX PF 29-AUG-2003; 2003WO-US027125.
XX PR 29-AUG-2002; 2002US-0407492P.
XX PA (CYTO-) CYTOCURE LLC.
XX

CC antimicrobial or cytostatic activity. In addition, the invention may
CCC prove useful for the production of a vaccine or for gene therapy. The
CCC composition and methods disclosed are useful for preventing or treating
CCC infectious diseases or cancer. The present sequence is that of a peptide
CCC which was used in the exemplification of the invention.

XX Sequence 9 AA;

SQ Query Match 100.0%; Score 51; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GLYDGEHL 9
|||||||
DB 1 GLYDGEHL 9

RESULT 11
AAY71489
ID AAY71489 standard; peptide; 10 AA.
XX AC
XX AC
XX DT
XX DT
XX DE
DE Human MAGE-A10 decapeptide-1.
XX DE
XX KW
KW HLA; Major Histocompatibility Complex; MHC; Human Leucocyte Antigen;
KW immune response stimulator; prophylaxis; therapy; diagnosis; tumour;
KW cancer; TNF; tumour necrosis factor; vaccine; cytostatic.
XX KW
XX OS Homo sapiens.
OS WO200032769-A2.
XX PN
PN 08-JUN-2000.
XX PD
PD 26-NOV-1999; 99WO-IB002018.
XX PF
PF 27-NOV-1998; 98GB-00026143.
XX PR
PR (LUDW-) LUDWIG INST CANCER RES.
XX PA
PA Huang L, Van Pel A, Brasseur F, De Plaen E, Boon T;
XX PI WPI; 2000-412317/35.
XX DR Novel polypeptides expressed in tumor cells useful for treating cancers
PT have an ability to complex with a major histocompatibility complex
PT molecule and comprises a specific unbroken amino acid sequence.
PT Claim 9; Page 37; 80pp; English.
PS The patent discloses MAGE-A10 and MAGE-A8 polypeptide, nonapeptide and
XX desapeptide sequences, that function as tumour rejection antigens (TRAs).
CC These peptides are capable of forming a complex with major
CC histocompatibility complex (MHC) molecule type HLA-A2.1 (Human Leucocyte
CC Antigen), that are recognised by T-lymphocytes and elicit an immune
CC response from cytolytic T-lymphocytes (CTL). They function as an immune
CC response stimulator. Tumour rejection antigens are useful in prophylaxis,
CC therapy and diagnosis of tumours and are effective in controlling or
CC preventing tumour growth. The present peptide sequence is the human MAGE-
CC A10 decapeptide-1, that corresponds to residues 254-263 of the MAGE-A10
CC protein. This peptide can serve as a tumour rejection antigen (TRA) and
CC in combination with adjuvants, can produce vaccines useful for treating a
CC variety of tumours that express MAGE-A10
XX SQ Sequence 10 AA;
Query Match 100.0%; Score 51; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0069;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLYDGMHL 9
 DB 1 GLYDGMHL 9

RESULT 12
 ADR69766
 ID ADR69766 standard; peptide; 20 AA.
 XX
 AC ADR69766;
 XX
 XX 18-NOV-2004 (first entry)
 XX
 DE Novel hybrid antigen-related peptide #1346.
 XX
 KW hybrid antigen; antigenic domain; infectious agent; tumour antigen;
 KW binding domain; heat shock protein; antimicrobial; cytostatic; vaccine;
 KW gene therapy; infectious disease; cancer.
 XX
 OS Unidentified.
 OS Synthetic.
 XX
 PN WO2004071457-A2.
 XX
 PD 26-AUG-2004.
 XX
 PF 13-FEB-2004; 2004WO-US004340.
 XX
 PR 13-FEB-2003; 2003US-0447142P.
 PR 11-APR-2003; 2003US-0462469P.
 PR 18-APR-2003; 2003US-0463746P.
 PR 16-SEP-2003; 2003US-0503417P.
 PR 12-FEB-2004; 2004US-00776521.
 XX
 PA (MOJVA-) MOJAVE THERAPEUTICS INC.
 XX
 XX Fletcher J, Prince-Cohane K, Mehta S, Slusarewicz P, Andjelic S;
 PI Barber B;
 XX
 XX WPI; 2004-625768/60.
 DR
 XX
 XX New hybrid antigens comprising an antigenic domain and improved heat
 PT shock protein-binding domains, useful for preventing or treating
 PT infectious diseases or cancer.
 XX
 XX Example 11; Page 44; 56pp; English.
 PS
 XX This invention relates to a novel hybrid antigen which comprises at least
 CC one antigenic domain of an infectious agent or tumour antigen and a
 CC binding domain that non-covalently binds to a heat shock protein. The
 CC invention may be useful for the production of compounds with an
 CC antimicrobial or cytostatic activity. In addition, the invention may
 CC prove useful for the production of a vaccine or for gene therapy. The
 CC composition and methods disclosed are useful for preventing or treating
 CC infectious diseases or cancer. The present sequence is that of a peptide
 CC which was used in the exemplification of the invention.
 XX
 XX Sequence 20 AA;
 SQ

Query Match 100.0%; Score 51; DB 8; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.015;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLYDGMHL 9
 DB 1 GLYDGMHL 9

RESULT 13
 AAY71485
 ID AAY71485 standard; protein; 369 AA.
 XX
 XX

AC AAY71485;
 XX
 DT 12-OCT-2000 (first entry)
 XX
 DE Human MAGE-A10 protein.
 XX
 KW MAGE-A10; human; Tumour Rejection Antigen; TRA; Human Leucocyte Antigen;
 KW HLA; Major Histocompatibility Complex; MHC; cytolytic T-lymphocyte; CTL;
 KW immune response stimulator; prophylaxis; therapy; diagnosis; tumour;
 KW cancer; TNF; tumour necrosis factor; cytostatic.
 XX
 OS Homo sapiens.
 OS
 PN WO2000032769-A2.
 XX
 PD 08-JUN-2000.
 XX
 PF 26-NOV-1999; 99WO-IB002018.
 XX
 PR 27-NOV-1998; 98GB-00026143.
 XX
 PA (LUDW-) LUDWIG INST CANCER RES.
 XX
 XX Huang L, Van Pel A, Brasseur F, De Plaen E, Boon T;
 PI
 XX WPI; 2000-412317/35.
 DR N-PSDB; AAD01311, AAD01312, AAD01313.
 XX
 PT Novel polypeptides expressed in tumor cells useful for treating cancers
 PT have an ability to complex with a major histocompatibility complex
 PT molecule and comprises a specific unbroken amino acid sequence.
 XX
 PS Claim 1; Fig 7; 80pp; English.
 XX
 CC The patent discloses MAGE-A10 and MAGE-A8 polypeptide, nonapeptide and
 CC decapeptide sequences, that function as tumour rejection antigens (TRAS).
 CC These peptides are capable of forming a complex with major
 CC histocompatibility complex (MHC) molecule type HLA-A2.1 (Human Leucocyte
 CC Antigen), that are recognised by T-lymphocytes and elicit an immune
 CC response from cytolytic T-lymphocytes (CTL). They function as an immune
 CC response stimulator. Tumour rejection antigens are useful in prophylaxis,
 CC therapy and diagnosis of tumours and are effective in controlling or
 CC preventing tumour growth. The present sequence is the human MAGE-A10
 CC protein, comprising nonapeptides and decapeptides, that serve as tumour
 CC rejection antigens (TRAS). The novel TRAS encoded by MAGE-A10 is
 CC identified using melanoma cell line (LS1731-MEL), stimulated by
 CC autologous CTL clone (447A/5) to produce TNF (tumour necrosis factor).
 CC Expression of MAGE-A10 has been detected in a variety of tumours like
 CC melanomas, carcinomas of the head and neck, bladder and prostate,
 CC myelomas and lung cancer. The only normal tissue expressing MAGE-A10 is
 CC the testis
 XX
 SQ Sequence 369 AA;
 Query Match 100.0%; Score 51; DB 3; Length 369;
 Best Local Similarity 100.0%; Pred. No. 0.34;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLYDGMHL 9
 DB 254 GLYDGMHL 262

RESULT 14
 AAB80297
 ID AAB80297 standard; protein; 369 AA.
 XX
 AC AAB80297;
 XX
 DT 24-APR-2001 (first entry)
 XX
 XX Human prostate cancer antigen #25.
 XX

KW Immunosuppressive; nootropic; neuroprotective; antiviral; vulnery;
 KW anticonvulsant; antibacterial; antifungal; antiparasitic; cardiac;
 KW immune disorder; cardiovascular disorder; neurological disease;
 KW infection; cancer; cytostatic; antiarthritic; antirheumatic;
 KW antiasthmatic; anticonvulsant; vasotropic; vulnery; human;
 KW secreted protein; prostate cancer antigen.

XX Homo sapiens.
 XX W0200107476-A1.
 XX 01-FEB-2001.
 XX 20-JUL-2000; 2000WO-US019666.
 XX 21-JUL-1999; 99US-0144972P.
 XX 13-AUG-1999; 99US-0148681P.
 XX 17-AUG-1999; 99US-0149173P.
 XX 06-OCT-1999; 99US-0158004P.
 XX 05-APR-2000; 2000US-0194689P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX (ROSE/) ROSEN C A.

XX Rosen CA, Birse C;
 XX WPI; 2001-138554/14.
 XX N-PSDB; AAF72765.
 XX New nucleic acid molecule encoding human secreted prostate cancer
 XX antigens, useful for the diagnosis and treatment of disorders such as
 XX cancer, leukemia and autoimmune disease.
 XX Claim 11; Page 399-400; 433pp; English.

CC The present invention relates to human secreted prostate cancer antigen
 CC coding sequences (AAF72741-AAF72789) and proteins (AAB80273-AAB80321).
 CC The coding sequences and proteins of the present invention are useful for
 CC preventing, treating or ameliorating a medical condition; and for the
 CC diagnosis and treatment of diseases and disorders. Diseases and disorders
 CC that can be diagnosed and treated include (auto)immune diseases (e.g.
 CC graft versus host disease and rheumatoid arthritis), inflammatory and
 CC allergic disorders (e.g. asthma), hyperproliferative disorders (e.g.
 CC cancers and leukemias), cardiovascular disorders (e.g. heart attacks and
 CC arrhythmias), cerebrovascular disorders (e.g. stroke), arterial occlusive
 CC disorders (e.g. arteriosclerosis), angiogenesis related disorders (e.g.
 CC retinopathy and keloid scars), ocular disorders (e.g. glaucoma),
 CC neurological disorders (e.g. Alzheimer's, Parkinson's disease, epilepsy
 CC and Creutzfeldt-Jakob disease) and infections caused by bacteria, fungi,
 CC viruses or parasites. They may also be useful for wound healing,
 CC epithelial cell proliferation, supporting cell culture, tissue
 CC regeneration, birth control and as a food additive or preservative

XX Sequence 369 AA;

Query Match 100.0%; Score 51; DB 4; Length 369;
 Best Local Similarity 100.0%; Pred. No. 0.34;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLYDGMHEHL 9
 |||||
 Db 254 GLYDGMHEHL 262

RESULT 15
 ABR48215
 ID ABR48215 standard; protein; 369 AA.
 XX AC ABR48215;

XX 12-JUN-2003 (first entry)
 XX Human bladder cancer associated protein sequence SEQ ID NO:149.

XX Human; bladder cancer; cytostatic; gene therapy; vaccine.
 KW Homo sapiens.
 XX W02003003906-A2.
 XX 16-JAN-2003.

XX 03-JUL-2002; 2002WO-US021338.
 XX 03-JUL-2001; 2001US-0302814P.
 XX 03-AUG-2001; 2001US-0310099P.
 XX 08-NOV-2001; 2001US-0343705P.
 XX 13-NOV-2001; 2001US-0350666P.
 XX 12-APR-2002; 2002US-0372246P.
 XX (BOSB-) EOS BIOTECHNOLOGY INC.

XX Mack DH, Aziz N;
 XX WPI; 2003-201532/19.
 XX N-PSDB; ACC51029.

XX Detecting a bladder cancer-associated transcript in a cell from a
 XX patient, comprises contacting a biological sample from the patient with a
 XX bladder cancer-associated polynucleotide or antibody.

XX Claim 10; Page 282; 307pp; English.

XX The present invention describes a method for detecting a bladder cancer-
 CC associated transcript in a cell from a patient. The method comprises
 CC contacting a biological sample from the patient with a polynucleotide
 CC that selectively hybridises to a sequence that is 80 % identical to a
 CC table of sequences (see ACC50951 to ACC51059). ACC50951 to ACC51059
 CC encode the human bladder cancer-associated proteins given in ABR48146 to
 CC ABR48242). Bladder cancer-associated sequences from the present invention
 CC have cytostatic activities, and can be used in antisense gene therapy and
 CC in vaccine production. The method can be used for detecting a bladder
 CC cancer-associated transcript in a cell from a patient. The method is
 CC useful in diagnosing or treating bladder cancer and in screening for
 CC compounds that modulate bladder cancer, such as hormones or antibodies.
 CC The nucleic acid molecules from the present invention may be used in
 CC various screening and diagnostic methods, and for gene therapy, vaccine
 CC and/or antisense/inhibition applications

XX Sequence 369 AA;

Query Match 100.0%; Score 51; DB 6; Length 369;
 Best Local Similarity 100.0%; Pred. No. 0.34;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLYDGMHEHL 9
 |||||
 Db 254 GLYDGMHEHL 262

Search completed: November 15, 2005, 15:40:01
 Job time : 7.69048 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 15, 2005, 15:32:22 ; Search time 1.2619 Seconds
(without alignments)
686.225 Million cell updates/sec

Title: US-09-856-812B-42
Perfect score: 51
Sequence: 1 GLYDGMHL 9
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79.*
1: Pir1.*
2: Pir2.*
3: Pir3.*
4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	51	100.0	369	2 I38659	melanoma antigen MAGE-10 - human
2	41	80.4	242	2 D40590	transcription initiation factor sigma, flagellar-specific - Vibrio parahaemolyticus
3	40	78.4	419	2 G72396	6-phosphofructokin
4	39	76.5	347	2 I38008	melanoma antigen M
5	39	76.5	389	2 S74343	probable aspartate
6	38	74.5	317	2 I38661	melanoma antigen M
7	36	70.6	237	2 S64718	formin-binding pro
8	36	70.6	425	2 H07933	hypothetical prote
9	36	70.6	575	2 A83486	hypothetical cytos
10	35	68.6	94	2 S26082	ribosomal protein
11	35	68.6	180	2 S57944	ADP-ribosylation f
12	35	68.6	180	2 A23741	ADP-ribosylation f
13	35	68.6	180	2 JC4949	ADP-ribosylation f
14	35	68.6	255	2 T35217	hypothetical prote
15	35	68.6	333	2 D89888	ornithine carbamoy
16	35	68.6	1172	2 D72482	probable antibioti
17	35	68.6	2163	2 S50675	pre-mRNA splicing
18	34	66.7	138	2 T49060	hypothetical prote
19	34	66.7	179	2 JH0260	ADP-ribosylation f
20	34	66.7	180	1 S37599	ADP-ribosylation f
21	34	66.7	181	2 B36167	ADP-ribosylation f
22	34	66.7	181	2 A36367	ADP-ribosylation f
23	34	66.7	182	2 C49993	ADP-ribosylation f
24	34	66.7	183	2 D49993	ADP-ribosylation f
25	34	66.7	205	2 D84537	probable ADP-ribos
26	34	66.7	241	2 AF0818	conserved hypotet
27	34	66.7	245	2 F69343	2-oxoacid-ferredox
28	34	66.7	248	2 G65035	probable DNA repli
29	34	66.7	248	2 B85893	probable DNA repli

30	34	66.7	248	2 F91048	probable DNA repli
31	34	66.7	333	2 A89999	sigmaB regulation
32	34	66.7	374	2 T06276	benzothiadiazole-1
33	34	66.7	388	2 AE2412	aspartate aminotra
34	34	66.7	405	2 T01136	hypothetical prote
35	34	66.7	433	2 F84235	hypothetical prote
36	34	66.7	434	2 F90184	cobyrinic acid A,C
37	34	66.7	472	2 B82492	tryptophanase (EC
38	34	66.7	476	1 WZEC	tryptophanase (imp
39	34	66.7	476	2 E91209	tryptophanase (imp
40	34	66.7	476	2 H86055	phosphate transpor
41	34	66.7	496	2 AF3500	prophage p13 prote
42	34	66.7	595	2 B86798	formate dehydrogen
43	34	66.7	782	2 B83966	probable coatomer
44	34	66.7	905	2 T38944	hypothetical prote
45	34	66.7	961	2 T23395	hypothetical prote

ALIGNMENTS

RESULT 1

I38659
melanoma antigen MAGE-10 - human
C;Species: Homo sapiens (man)
C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004
C;Accession: I38659
R;De Plaen, B.; Arden, K.; Traversari, C.; Gaforio, J.J.; Szikora, J.P.; De Smet, C.; Bm
oon, T.
Immunogenetics 40, 360-369, 1994
A;Title: Structure, chromosomal localization, and expression of 12 genes of the MAGE fam
A;Reference number: I38659; MUID:95012457; PMID:7927540
A;Accession: I38659
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-369 <RES>
A;Cross-references: UNIPROT:P43363; EMBL:U10685; NID:G533510; PIDN:AAA68869.1; PID:G53353
C;Genetics:
A;Gene: GDB:MAGEA10; MAGE10
A;Cross-references: GDB:331126
A;Map position: Xq28-Xq28
A;Introns: #status absent
C;Superfamily: tumor associated protein MAGE

Query Match 100.0%; Score 51; DB 2; Length 369;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLYDGMHL 9
|||
Db 254 GLYDGMHL 262

RESULT 2

D40590
transcription initiation factor sigma, flagellar-specific - Vibrio parahaemolyticus
C;Species: Vibrio parahaemolyticus
C;Date: 12-May-1994 #sequence_revision 12-May-1994 #text_change 09-Jul-2004
C;Accession: D40590
R;McCarter, L.L.; Wright, M.E.
J. Bacteriol. 175, 3361-3371, 1993
A;Title: Identification of genes encoding components of the swarmer cell flagellar motor
A;Reference number: A40590; MUID:93273702; PMID:8501040
A;Accession: D40590
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-242 <MCC>
A;Cross-references: UNIPROT:Q03474; GB:U20541; GB:L06177; NID:G677906; PIDN:AAA62353.1; PID:G53353
C;Genetics:
A;Gene: lafs
C;Superfamily: transcription initiation factor sigmaD; transcription initiation factor sigma
C;Keywords: DNA binding; sigma factor; transcription initiation

Query Match 80.4%; Score 41; DB 2; Length 242;
 Best Local Similarity 87.5%; Pred. No. 1.5;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLYDGMHL 8
 Db 172 GQYDGMHL 179
 |||||
 |||||

RESULT 3
 G72396
 6-phosphofructokinase, pyrophosphate-dependent - Thermotoga maritima (strain MSB8)
 C;Species: Thermotoga maritima
 C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
 C;Accession: G72396
 R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
 Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
 C.M.
 Nature 399, 323-329, 1999
 A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
 A;Reference number: A72200; MUID:99287316; PMID:10360571
 A;Accession: G72396
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-419 <ARN>
 A;Cross-references: UNIPROT:Q9WYC5; GB:AE001710; GB:AE000512; NID:94980775; PIDN:AAD3537
 A;Experimental source: strain MSB8
 C;Genetics:
 A;Gene: TM0289
 C;Superfamily: pyrophosphate-dependent phosphofructokinase, TM0289 type; 6-phosphofructo

Query Match 78.4%; Score 40; DB 2; Length 419;
 Best Local Similarity 66.7%; Pred. No. 4.4;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLYDGMHL 9
 Db 37 GYDGPRL 45
 :|||:|
 :|||:|

RESULT 4
 I38008
 melanoma antigen MAGE-B1 - human
 N;Alternate names: MAGE-Xp protein; MAGE-like protein 1
 C;Species: Homo sapiens (man)
 C;Date: 01-Mar-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
 C;Accession: I38008; S52167
 R;Muscatelli, F.; Walker, A.P.; De Plaen, E.; Stafford, A.N.; Monaco, A.P.
 Proc. Natl. Acad. Sci. U.S.A. 92, 4987-4991, 1995
 A;Title: Isolation and characterization of a MAGE gene family in the Xp21.3 region.
 A;Reference number: I38008; MUID:95281581; PMID:7761436
 A;Accession: I38008
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-347 <RES>
 A;Cross-references: UNIPROT:Q96TG1; EMBL:X82539; NID:9608992; PIDN:CAA57889.1; PID:96089
 C;Genetics:
 A;Gene: GDB:MAGEB1; MAGE1; MAGE-Xp
 A;Cross-references: GDB:635712; OMIM:600619
 A;Map position: Xp21.3-Xp21.3
 C;Superfamily: tumor associated protein MAGE

Query Match 76.5%; Score 39; DB 2; Length 347;
 Best Local Similarity 77.8%; Pred. No. 5.7;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GLYDGMHL 9
 Db 228 GAYDGEHL 236
 |||||
 |||||

RESULT 5
 S74343

probable aspartate transaminase (EC 2.6.1.1) aspC sl10402 [similarity] - Synechocystis sp.
 N;Alternate names: hypothetical protein sl10402
 C;Species: Synechocystis sp.
 A;Variety: PCC 6803
 C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
 C;Accession: S74343
 R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
 O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda,
 DNA Res. 3, 109-136, 1996
 A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
 sp.
 A;Reference number: S74322; MUID:97061201; PMID:8905231
 A;Accession: S74343
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: RNA
 A;Residues: 1-389 <KAN>
 A;Cross-references: UNIPROT:Q55128; EMBL:D64001; GB:AB001339; NID:91001102; PIDN:BAAL0263
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
 C;Genetics:
 A;Gene: aspC
 C;Superfamily: aspartate transaminase
 C;Keywords: aminotransferase; phosphoprotein; pyridoxal phosphate
 F;238/Binding site: pyridoxal phosphate (Lys) (covalent) #status Predicted

Query Match 76.5%; Score 39; DB 2; Length 389;
 Best Local Similarity 87.5%; Pred. No. 6.5;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LYDGMHL 9
 Db 210 LYDGMHL 217
 |||||
 |||||

RESULT 6
 I38661
 melanoma antigen MAGE-4 - human
 N;Alternate names: MAGE 41 protein; melanoma antigen MAGE-X2
 C;Species: Homo sapiens (man)
 C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004
 C;Accession: I38661; PH1297; PH1298; JC2359; G01446
 R;De Plaen, E.; Arden, K.; Traversari, C.; Gaforio, J.J.; Szikora, J.P.; De Smet, C.; B
 oon, T.
 Immunogenetics 40, 360-369, 1994
 A;Title: Structure, chromosomal localization, and expression of 12 genes of the MAGE fam
 A;Reference number: I38659; MUID:95012457; PMID:7927540
 A;Accession: I38661
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-317 <DBP1>
 A;Cross-references: UNIPROT:P43358; EMBL:U10687; NID:9533514; PIDN:AAA68871.1; PID:95335
 A;Experimental source: antigen MAGE-4a
 A;Accession: I38662
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-172, 'T', 174-317 <DEP2>
 A;Cross-references: EMBL:U10688; NID:9533516; PIDN:AAA68872.1; PID:9533517
 A;Experimental source: antigen MAGE-4b
 R;Traversari, C.; van der Bruggen, P.; Luescher, I.F.; Lurquin, C.; Chomez, P.; Van Pel,
 J. Exp. Med. 176, 1453-1457, 1992
 A;Title: A nonapeptide encoded by human gene MAGE-1 is recognized on HLA-A1 by cytolytic
 A;Reference number: PH1294; MUID:93018875; PMID:1402688
 A;Accession: PH1297
 A;Molecule type: DNA
 A;Residues: 169-172, 'T', 174-177 <TRA2>
 A;Experimental source: antigen MAGE-41
 R;Ding, M.; Beck, R.J.; Keller, C.J.; Fenton, R.G.
 Biochem. Biophys. Res. Commun. 202, 549-555, 1994
 A;Title: Cloning and analysis of MAGE-1-related genes.
 A;Reference number: JC2358; MUID:94311935; PMID:8037761

A;Accession: JC2359
A;Molecule type: mRNA
A;Residues: 1-172, 'T', 174-306, 'Q', 308-317 <DIN>
A;Cross-references: EMBL:U10340; NID:g499123; PIDN:AAAL19007.1; PID:g499124
A;Experimental source: melanoma cell line DM150
C;Genetics:
A;Gene: GDB:MAGE4; MAGE4; MAGE-X2
A;Cross-references: GDB:331119
A;Map position: Xq28-Xq28
A;Introns: #status absent
C;Superfamily: tumor associated protein MAGE
F;169-177/Region: HLA-A1 binding #status predicted

Query Match 74.5%; Score 38; DB 2; Length 317;
Best Local Similarity 75.0%; Pred. No. 8.1;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLYDGMHEH 8
|:|||||
DB 230 GYVDGREH 237

RESULT 7
S64718
formin-binding protein 17 - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S64718; S64711
R;Chan, D.C.; Bedford, M.T.; Leder, P.
submitted to the EMBL Data Library, November 1995
A;Reference number: S64718
A;Accession: S64718
A;Molecule type: mRNA
A;Residues: 1-237 <CHA>
A;Cross-references: UNIPROT:Q61053; EMBL:U40751; NID:g1255032; PIDN:AACS2479.1; PID:g1255032
R;Chan, D.C.; Bedford, M.T.; Leder, P.
EMBO J. 15, 1045-1054, 1996
A;Title: Formin binding proteins bear WWP/WF domains that bind proline-rich peptides and
A;Reference number: S64711; MUID:96183189; PMID:8605874
A;Accession: S64711
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 170-191, 'S', 193-205, 'P', 207-216, 'V', 218-222 <CHW>
A;Cross-references: EMBL:U40751
P;173-222/Domain: SH3 homology <SH3>

Query Match 70.6%; Score 36; DB 2; Length 237;
Best Local Similarity 75.0%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GLYDGMHEH 8
|:|||||
DB 114 GLYDQTH 121

RESULT 8
H70793
hypothetical protein Rv3703c - Mycobacterium tuberculosis (strain H37Rv)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: H70793
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Squares, R.; Sulston, J.B.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: H70793
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-425 <COL>
A;Cross-references: UNIPROT:O69671; GB:AL022121; GB:AL123456; NID:g3261559; PIDN:CAA1802

A;Experimental source: strain H37Rv
A;Genetics:
A;Gene: Rv3703c

Query Match 70.6%; Score 36; DB 2; Length 425;
Best Local Similarity 75.0%; Pred. No. 29;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GLYDGMHEH 8
|:|||||
DB 73 GLYDAFEH 80

RESULT 9
AE3486
hypothetical cytosolic protein BMEI1875 [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: AE3486
R;DelVecchio, V.G.; Kaputal, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, I.; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagijs, S.; O'Callaghan, D.; Letesee
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
A;Reference number: AD3252; PMID:11756688
A;Accession: AE3486
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-575 <KUR>
A;Cross-references: UNIPROT:Q8YEK3; GB:AE008917; PIDN:AAL53056.1; PID:g17983917; GSPDB:Q2
A;Experimental source: strain 16M
C;Genetics:
A;Gene: BMEI1875
A;Map position: 1

Query Match 70.6%; Score 36; DB 2; Length 575;
Best Local Similarity 75.0%; Pred. No. 41;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GLYDGMHEH 8
|:|||||
DB 558 GLYDGNH 565

RESULT 10
S26082
ribosomal protein S19 - Euglena gracilis chloroplast
C;Species: Chloroplast Euglena gracilis
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: S26082; S34522; S34889
R;Christopher, D.A.; Cushman, J.C.; Price, C.A.; Hallick, R.B.
Curr. Genet. 14, 275-286, 1988
A;Title: Organization of ribosomal protein genes rpl23, rpl2, rps19, rpl22 and rps3 on t
A;Reference number: S26080; MUID:89063445; PMID:3143485
A;Accession: S26082
A;Molecule type: DNA
A;Residues: 1-94 <CHR>
A;Cross-references: UNIPROT:P19170; EMBL:Z11874; NID:g14353; PIDN:CAA77918.1; PID:g14368
R;Hallick, R.B.; Hong, L.; Drager, R.G.; Favreau, M.; Monfort, A.; Orsat, B.; Spielmann,
submitted to the EMBL Data Library, January 1993
A;Description: The complete sequence of the Euglena gracilis chloroplast genome (tentati
A;Reference number: S34494
A;Accession: S34522
A;Molecule type: DNA
A;Residues: 1-94 <HAL1>
A;Cross-references: EMBL:X70810; NID:g415327; PIDN:CAA50101.1; PID:g415757
R;Hallick, R.B.; Hong, L.; Drager, R.G.; Favreau, M.R.; Monfort, A.; Orsat, B.; Spielmann,
Nucleic Acids Res. 21, 3537-3544, 1993
A;Title: Complete sequence of Euglena gracilis chloroplast DNA.
A;Reference number: S34862; MUID:93347989; PMID:8346031
A;Accession: S34889
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-94 <HAL2>

A;Cross-references: EMBL:X70810; NID:g415327; PIDN:CAA50101.1; PID:g415757
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1993
C;Genetics:
A;Gene: rps19
A;Genome: chloroplast
A;Introns: 26/3; 69/3
C;Superfamily: ribosomal protein S19/S15
C;Keywords: chloroplast; protein biosynthesis; ribosome

Query Match 68.6%; Score 35; DB 2; Length 94;
Best Local Similarity 55.6%; Pred. No. 7.8;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLYDGMHKL 9
|:|:|:|:
Db 50 GYNGKEHI 58

RESULT 11
S57944
ADP-ribosylation factor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
C;Accession: S57944
R;Konkel, D.A.; Song, S.K.
submitted to the EMBL Data Library, October 1990
A;Description: Nucleotide sequence of a putative chicken ADP-ribosylation factor cDNA.
A;Reference number: S57944
A;Accession: S57944
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-180 <KON>
A;Cross-references: UNIPROT:P49702; EMBL:X55998; NID:g899263; PIDN:CAA39470.1; PID:g8992
C;Superfamily: ADP-ribosylation factor
C;Keywords: blocked amino end; lipoprotein; myristylation; nucleotide binding; P-loop
F;24-31/Region: nucleotide-binding motif A (P-loop)
F;89-94/Region: nucleotide-binding motif B
F;126-129/Region: GTP-binding NKXD motif
F;126-129/Region: GTP-binding NKXD motif
F;126-129/Region: GTP-binding NKXD motif

Query Match 68.6%; Score 35; DB 2; Length 180;
Best Local Similarity 66.7%; Pred. No. 17;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLYDGMHKL 9
|:|:|:|:
Db 165 GLYDGLDWL 173

RESULT 12
A23741
ADP-ribosylation factor 5 - human
C;Species: Homo sapiens (man)
C;Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 09-Jul-2004
C;Accession: A23741
R;Teuchiya, M.; Price, S.R.; Teai, S.C.; Moss, J.; Vaughan, M.
J. Biol. Chem. 266, 2772-2777, 1991
A;Title: Molecular identification of ADP-ribosylation factor mRNAs and their expression
A;Reference number: A23741; MUID:91131565; PMID:1993656
A;Accession: A23741
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-180 <TSU>
A;Cross-references: UNIPROT:P26437; GB:M57567; NID:g178986; PIDN:AAA90927.1; PID:g178987
C;Genetics:
A;Gene: GDB:ARF5
A;Cross-references: GDB:136902; OMIM:103188
A;Map position: 17q12-17q21
C;Superfamily: ADP-ribosylation factor
C;Keywords: blocked amino end; lipoprotein; myristylation; nucleotide binding; P-loop
F;24-31/Region: nucleotide-binding motif A (P-loop)
F;89-94/Region: nucleotide-binding motif B
F;126-129/Region: GTP-binding NKXD motif

F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted

Query Match 68.6%; Score 35; DB 2; Length 180;
Best Local Similarity 66.7%; Pred. No. 17;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLYDGMHKL 9
|:|:|:|:
Db 165 GLYDGLDWL 173

RESULT 13
JC4949
ADP-ribosylation factor 5 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 09-Jul-2004
C;Accession: JC4949
R;Hosaka, M.; Toda, K.; Takatsu, H.; Torii, S.; Murakami, K.; Nakayama, K.
J. Biochem. 120, 813-819, 1996
A;Title: Structure and intracellular localization of mouse ADP-ribosylation factors type
A;Reference number: JC4945; MUID:97103475; PMID:8947846
A;Accession: JC4949
A;Molecule type: mRNA
A;Residues: 1-180 <HOS>
A;Cross-references: UNIPROT:P26437; DDBJ:D87902; NID:g1565214; PIDN:BAAL3494.1; PID:g156
A;Experimental source: brain
C;Comment: This protein belongs to class II of ADP-ribosylation factors which are a fami
C;Superfamily: ADP-ribosylation factor
C;Keywords: blocked amino end; lipoprotein; myristylation; nucleotide binding; P-loop
F;24-31/Region: nucleotide-binding motif A (P-loop)
F;89-94/Region: nucleotide-binding motif B
F;126-129/Region: GTP-binding NKXD motif
F;126-129/Region: GTP-binding NKXD motif
F;126-129/Region: GTP-binding NKXD motif

Query Match 68.6%; Score 35; DB 2; Length 180;
Best Local Similarity 66.7%; Pred. No. 17;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLYDGMHKL 9
|:|:|:|:
Db 165 GLYDGLDWL 173

RESULT 14
T35217
hypothetical protein SC5C7.10c SC5C7.10c - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C;Accession: T35217
R;Seeger, K.J.; Harris, D.; Parkhill, J.; Barrall, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, September 1998
A;Reference number: Z21572
A;Accession: T35217
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-255 <SEE>
A;Cross-references: UNIPROT:O86707; EMBL:AL031515; PIDN:CAA20622.1; GSPDB:GN00070; SCOE
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOE:SC5C7.10c
C;Superfamily: conserved hypothetical protein MJ1163

Query Match 68.6%; Score 35; DB 2; Length 255;
Best Local Similarity 85.7%; Pred. No. 25;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLYDGMHKL 7
|:|:|:|:
Db 151 GLFDGME 157

RESULT 15
D89888

ornithine carbamoyltransferase [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: D89888
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogud
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: D89888
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-333 <KUR>
A;Cross-references: UNIPROT:Q9K3A1; GB:BA000018; PID:gl3700968; PIDN:BA042264.1; GSPDB:G
A;Experimental source: strain N315
C;Genetics:
A;Gene: argP
C;Superfamily: ornithine carbamoyltransferase; aspartate/ornithine carbamoyltransferase

Query Match 68.6%; Score 35; DB 2; Length 333;
Best Local Similarity 62.5%; Pred. No. 34;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLYDGMH 8
|:|:|:|:
Db 99 GMYDGIEY 106

Search completed: November 15, 2005, 15:44:46
Job time : 3.2619 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 15, 2005, 15:31:39 ; Search time 5.2619 Seconds
(without alignments)
875.864 Million cell updates/sec

Title: US-09-856-812B-42
Perfect score: 51
Sequence: 1 GLYDGMHL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	369	1	MAGA_HUMAN
2	43	84.3	347	2	Q96L22
3	42	82.4	330	2	Q8ECU8
4	41	80.4	242	1	LAFS_VIBPA
5	41	80.4	318	2	Q8BUN9
6	40	78.4	340	2	Q97AP7
7	40	78.4	419	2	Q9WYC5
8	39	76.5	347	1	MGB1_HUMAN
9	39	76.5	347	2	Q96CW8
10	39	76.5	347	2	Q96TC1
11	39	76.5	347	2	Q8FHJ0
12	39	76.5	378	2	Q9TTV4
13	39	76.5	387	2	Q8DGG0
14	39	76.5	389	1	AAT_SYNY3
15	39	76.5	394	2	Q94EG1
16	38	74.5	202	2	Q67SK0
17	38	74.5	317	1	MAGA_HUMAN
18	38	74.5	327	2	Q14798
19	38	74.5	328	2	Q6L129
20	38	74.5	346	1	MGB4_HUMAN
21	38	74.5	346	2	Q81Z00
22	37	72.5	214	2	Q8KY15
23	37	72.5	224	1	RNFE_PASNU
24	37	72.5	319	1	MGB2_HUMAN
25	37	72.5	334	2	Q9HKU8
26	37	72.5	347	2	Q8S9Y6
27	37	72.5	392	2	Q7NG02
28	37	72.5	429	2	Q8D4D2
29	37	72.5	444	2	Q8R659
30	37	72.5	487	2	Q9ACU1
31	37	72.5	864	1	AM11_ENCCU

32	37	72.5	864	1	AM12_ENCCU
33	37	72.5	1390	1	RPOB_MYCGA
34	36	70.6	237	2	Q6G0E7
35	36	70.6	237	2	Q61053
36	36	70.6	247	2	Q8SVW0
37	36	70.6	397	2	Q67QM8
38	36	70.6	425	2	Q7D513
39	36	70.6	425	2	Q69671
40	36	70.6	425	2	Q7TW2
41	36	70.6	440	2	Q8GPN8
42	36	70.6	441	2	Q7N1R6
43	36	70.6	476	2	Q6FAL7
44	36	70.6	483	2	Q8G380
45	36	70.6	539	2	Q8EJL4

Q8xg3 encephalito
P47715 mycoplasma
Q6g0e7 bartonella
Q61053 mus musculus
Q8svw0 encephalito
Q67qm8 symbiobacte
Q7d513 mycobacteri
Q69671 mycobacteri
Q7tw2 mycobacteri
Q8gpn8 streptomyce
Q7n1r6 photorhabdu
Q6fal7 acinetobact
Q8g380 brucella su
Q8ejl4 shewanella

ALIGNMENTS

RESULT 1

ID	MAGA_HUMAN	STANDARD	PRT	369 AA
AC	P43363			
DT	01-NOV-1995 (Rel. 32, Created)			
DT	01-NOV-1995 (Rel. 32, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Melanoma-associated antigen 10 (MAGE-10 antigen).			
GN	Name=MAGEA10; Synonyms=MAGE10;			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=95012457; PubMed=7927540;			
RA	de Plaen E., Arden K., Traversari C., Gaforio J.J., Szikora J.-P.,			
RA	de Smet C., Brasseur P., van der Bruggen P., Lethe B., Lurquin C.,			
RA	Brasseur R., Chomez P., de Backer O., Cavenne W., Boon T.;			
RT	"Structure, chromosomal localization, and expression of 12 genes of			
RT	the MAGE family.";			
RL	Immunogenetics 40:360-369(1994).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Skin;			
RX	MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,			
RA	Boeak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalley D.E.,			
RA	Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
CC	-/- FUNCTION: Not known, though may play a role in embryonal			
CC	development and tumor transformation or aspects of tumor			
CC	progression.			
CC	-/- TISSUE SPECIFICITY: Expressed in many tumors of several types,			
CC	such as melanoma, head and neck squamous cell carcinoma, lung			
CC	carcinoma and breast carcinoma, but not in normal tissues except			
CC	for testes and placenta.			
CC	-/- SIMILARITY: Contains 1 MAGE domain.			

```

-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
-----
DR EMBL; UI0689; AAA68869.1; -.
DR EMBL; BC004105; AAH04105.1; -.
DR PIR; I38659; I38659.
DR Genew; HGNC:6797; MAGEA10.
DR H-InvDB; HIX0017116; -.
DR MIM; 300343; -.
DR InterPro; IPR002190; MAGE.
DR Pfam; PF01454; MAGE; 1.
DR PROSITE; PS0838; MAGE; 1.
KW Antigen; Multigene family; Tumor antigen.
FT DOMAIN 134 333
FT DOMAIN 54 62 Poly-Ser.
SQ SEQUENCE 369 AA; 40766 MW; 16FA3301CAB716A6 CRC64;
-----
Query Match 100.0%; Score 51; DB 1; Length 369;
Best Local Similarity 100.0%; Pred. No. 0.44;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLYDGMH 9
Db 254 GLYDGMH 262

RESULT 2
ID Q96L22 PRELIMINARY; PRT; 347 AA.
AC Q96L22;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein FLJ32965.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-testis;
RX PubMed=14702039; DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Ohyaashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
RA Ninomiya K., Ishibashi T., Yanashita H., Murakawa K., Fujimori K.,
RA Tanai H., Kinata M., Watanabe M., Hiraoa S., Chiba Y., Ishida S.,
RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,
RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Moriya S., Moniyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,

```

```

RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs."
RL Nat. Genet. 36:40-45(2004).
DR EMBL; AK057527; BAB71522.1; -.
DR InterPro; IPR002190; MAGE.
DR Pfam; PF01454; MAGE; 1.
DR PROSITE; PS0838; MAGE; 1.
SQ SEQUENCE 347 AA; 38878 MW; 3B52411D840D873F CRC64;
-----
Query Match 84.3%; Score 43; DB 2; Length 347;
Best Local Similarity 87.5%; Pred. No. 13;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLYDGMH 8
Db 231 GLYDGMH 238

RESULT 3
ID Q8ECU8 PRELIMINARY; PRT; 330 AA.
AC Q8ECU8;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein SO3025.
GN OrderedLocusNames=SO3025;
OS Shewanella oneidensis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Shewanellaceae; Shewanella.
OX NCBI_TaxID=70863;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MR-1;
RX MEDLINE=22297686; PubMed=12368813; DOI=10.1038/nbt749;
RA Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,
RA Read T.D., Eisen J.A., Seshadri R., Ward N.L., Methe B.A.,
RA Clayton R.A., Meyer T., Teapin A., Scott J., Beanan M.J.,
RA Brinkac L.M., Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S.,
RA Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A.,
RA White O., Wolf A.M., Vamathevan J.J., Weidman J.F., Impraim M.,
RA Lee K., Berry K.J., Lee C., Mueller J., Khouri H.M., Gill J.,
RA Utterback T.R., McDonald L.A., Feldblym T.V., Smith H.O.,
RA Venter J.C., Neilson K.H., Fraser C.M.;
RT "Genome sequence of the dissimilatory metal ion-reducing bacterium
RT Shewanella oneidensis."
RL Nat. Biotechnol. 20:1118-1123(2002).
DR EMBL; AE015739; AAN56037.1; -.
DR TIGR; SO3025; -.
DR InterPro; IPR008001; Esterase_put.
DR Pfam; PF00756; Esterase; 1.
KW Complete proteome.
SQ SEQUENCE 330 AA; 37462 MW; 9B2F0235AF427242 CRC64;
-----
Query Match 82.4%; Score 42; DB 2; Length 330;
Best Local Similarity 77.8%; Pred. No. 18;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLYDGMH 9
Db 253 GLYDGMH 261

RESULT 4
ID LAFS_VIBPA STANDARD; PRT; 242 AA.
AC Q03474;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)

```

DE RNA polymerase sigma factor for flagellar operon (Sigma-F factor)
 GN (Sigma-27).
 DE Name=JafS; OrderedLocusNames=VPA1555;
 OS Vibrio parahaemolyticus.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 CC Vibrionaceae; Vibrrio.
 OX NCBI_TaxID=670;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=BB22;
 RC STRAIN=92273702; PubMed=8501040;
 RX MEDLINE=92273702; PubMed=8501040;
 RA McCarter L.L., Wright M.E.;
 RT "Identification of genes encoding components of the swarmer cell
 RT flagellar motor and propeller and a sigma factor controlling
 RT differentiation of Vibrio parahaemolyticus";
 RL J. Bacteriol. 175:3361-3371(1993).
 RN [2]
 RN SEQUENCE FROM N.A.
 RP STRAIN=RIND 2210633 / Serotype O3:K6;
 RC MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;
 RX Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
 RA Iijima Y., Nishina M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
 RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
 RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
 RT distinct from that of V. cholerae";
 RL Lancet 361:743-749(2003).
 CC -1- FUNCTION: Sigma factors are initiation factors that promote the
 CC attachment of RNA polymerase to specific initiation sites and are
 CC then released. This alternative sigma factor is specific for the
 CC flagellin gene (fliC) expression.
 CC -1- INDUCTION: Under conditions in which the polar flagellum is not
 CC functional.
 CC -1- SIMILARITY: Belongs to the sigma-70 factor family.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; U20541; AAA62353.1; -;
 CC EMBL; U52957; AAB07356.1; -;
 CC EMBL; AP005089; BAC62898.1; -;
 CC PIR; D40590; D40590.
 CC InterPro; IPR009043; RNA_pol_sigma.
 CC InterPro; IPR007627; Sigma70_r2.
 CC InterPro; IPR007630; Sigma70_r4.
 CC InterPro; IPR000943; Sigma70.
 CC Pfam; PF04542; Sigma70_r2; 1.
 CC Pfam; PF04545; Sigma70_r4; 1.
 CC PRINTS; PR00046; SIGMA70PCT.
 CC PROSITE; PS00715; SIGMA70_1; FALSE_NEG.
 CC PROSITE; PS00716; SIGMA70_2; 1.
 CC Complete proteome; DNA-binding; DNA-directed RNA polymerase;
 CC Sigma factor; Transcription regulation.
 CC DOMAIN 55 68 Polymerase core binding (Potential).
 CC PROSITE; PS00716; SIGMA70_2; 1.
 CC H-T-H motif (By similarity).
 FT DNA_BIND 211 230
 FT SEQUENCE 242 AA; 27835 MW; 39A3C7152DE2FC95 CRC64;
 Query Match 80.4%; Score 41; DB 1; Length 242;
 Best Local Similarity 87.5%; Pred. No. 21;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 GLYDGMH 8
 Db 172 QYDGMH 179
 RESULT 5
 Q9BUN9 PRELIMINARY; PRT; 318 AA.
 ID Q9BUN9

AC Q9BUN9;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Melanoma antigen, family A, 8.
 GN Names=WAGEA8;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Skin;
 RX MEDLINE=223388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler N.G.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haile F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uadin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S.K., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Whiting J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalley D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Skin;
 RX Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RN SEQUENCE FROM N.A.
 RP Kalline N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
 RA Koundinya M., Raphael J., Moreira D., Kelley T., Labaer J., Lin Y.,
 RA Phelan M., Farmer A.;
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Skin;
 RX Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 RL EMBL; BC002455; AAH02455.1; -;
 DR EMBL; BC007340; AAF36004.1; -;
 DR EMBL; BT007340; AAF36004.1; -;
 DR EMBL; BC012744; AAH12744.1; -;
 DR InterPro; IPR002190; MAGE.
 DR Pfam; PF01454; MAGE; 1.
 DR PROSITE; PS0838; MAGE; 1.
 SQ SEQUENCE 318 AA; 35214 MW; EA02C1FB42F6C080 CRC64;
 Query Match 80.4%; Score 41; DB 2; Length 318;
 Best Local Similarity 87.5%; Pred. No. 27;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 GLYDGMH 8
 Db 232 GLYDGMH 239
 RESULT 6
 Q97AP7 PRELIMINARY; PRT; 340 AA.
 ID Q97AP7
 AC Q97AP7; 2001 (TrEMBLrel. 18, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)

```

DT 01-JUN-2003 (TreeBLrel. 24, Last annotation update)
DE Threonine synthase.
GN Name=TV0766521; OrderedLocusNames=TV0763;
OS Thermoplasma volcanium.
OC Archaea; Euryarchaeota; Thermoplasmatata; Thermoplasmatales;
OC Thermoplasmataceae; Thermoplasma.
OX NCBI_TaxID=50339;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GS81 / DSM 4299 / JCM 9571;
RX MEDLINE=20570466; PubMed=11121031; DOI=10.1073/pnas.97.26.14257;
RA Kawashima T., Amano N., Koike H., Makino S.-I., Higuchi S.,
RA Kawashima-Obiya Y., Watanabe K., Yamazaki M., Kanehori K., Kawamoto T.,
RA Nunoshiba T., Yanamoto Y., Aramaki H., Makino K., Suzuki M.;
RT "Archaeal adaptation to higher temperatures revealed by genomic
sequence of Thermoplasma volcanium."
RL Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000).
DR EMBL; AP000993; BAB59905.1; -.
DR HSP; Q9WZD3; 1058.
DR GO; GO:0016829; F-lyase activity; IEA.
DR GO; GO:0006520; P:amino acid metabolism; IEA.
DR InterPro; IPR001926; B6_enzyme_beta.
DR Pfam; PF00291; PALP; 1.
KW Complete proteome; Pyridoxal phosphate.
SQ SEQUENCE 340 AA; 37877 MW; FC2864128896433B CRC64;

Query Match 78.4%; Score 40; DB 2; Length 340;
Best Local Similarity 77.8%; Pred. No. 44;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GLYDGMHL 9
DB 213 GLYSGFEHL 221

RESULT 7
Q9WYCS PRELIMINARY; PRT; 419 AA.
AC Q9WYCS;
DT 01-NOV-1999 (TreeBLrel. 12, Created)
DT 01-NOV-1999 (TreeBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TreeBLrel. 24, Last annotation update)
DE 6-phosphofructokinase, pyrophosphate-dependent.
GN OrderedLocusNames=TW0289;
OS Thermotoga maritima.
OC Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
OX NCBI_TaxID=23336;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MSB8 / DSM 3109 / ATCC-43589;
RX MEDLINE=99287316; PubMed=10360571; DOI=10.1038/20601;
RA Nelson K.E., Clayton R.A., Gill S.R., Gwin M.L., Dodson R.J.,
RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
RA McDonald L.A., Uterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.L.,
RA Heidelberg J.F., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT "Evidence for lateral gene transfer between Archaea and Bacteria from
genome sequence of Thermotoga maritima."
RL Nature 393:323-329(1999).
DR EMBL; AE001710; AAD35377.1; -.
DR PIR; G72396; G72396.
DR HSP; P70826; 1K2H.
DR TIGR; TW0289; -.
DR GO; GO:0005945; C:6-phosphofructokinase complex; IEA.
DR GO; GO:0003872; F:6-phosphofructokinase activity; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0006096; P:glycolysis; IEA.
DR InterPro; IPR000023; PfFructkinase.
DR Pfam; PF00365; PFK; 1.
DR PIRSF; PIRSF036482; PPI_PFK_TM0289; 1.
DR PRINTS; PR00476; PFRCTKINASE.

```

```

DR ProDom: PD000707; Ppfuckinase; 1.
KW Complete proteome; Kinase.
SQ SEQUENCE 419 AA; 46464 MW; 4E3FBC75A8410CEC CRC64;

Query Match 78.4%; Score 40; DB 2; Length 419;
Best Local Similarity 66.7%; Pred. No. 54;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLYDGMHL 9
DB 37 GYVDGPKHL 45

RESULT 8
MGBI_HUMAN STANDARD; PRT; 347 AA.
ID MGBI_HUMAN
AC P43366; O00601; O75862;
DT 01-NOV-1995 (Rel. 32, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Melanoma-associated antigen B1 (MAGE-B1 antigen) (MAGE-XP antigen)
DE (DSS-AHC critical interval MAGE superfamily 10) (DAM10).
GN Name=MAGEB1; Synonyms=MAGEB1, MAGEXP;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=95281581; PubMed=7761436;
RA Muscatelli F., Walker A.P., de Plaen E., Stafford A.N., Monaco A.P.;
RT "Isolation and characterization of a MAGE gene family in the xp21.3
region."
RL Proc. Natl. Acad. Sci. U.S.A. 92:4987-4991(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=96081328; PubMed=8535061;
RA Dabovic B., Zanaria E., Bardon B., Lisa A., Bordignon C., Russo V.,
RA Matesi C., Traversari C., Camerino G.;
RT "A family of rapidly evolving genes from the sex reversal critical
region in Xp21."
RL Mamm. Genome 6:571-580(1995).
RN [3]
RP SEQUENCE FROM N.A.
RA Muzny D., Aronson A.D., Adams C., Brundage E., Bunac C., Carvelli K.,
RA Chacko J., Chen J., Di W., Ding Y., Dugan S., Durbin J., Forcum J.,
RA Ganesh R., Garcia C., Goodman M., Gorrell J.H., Haywood M.,
RA Hernandez J., Jackson L., Jin S., Kampal R., Karpathy S., Kovar C.,
RA Leal B., Li Y., Lichtarge O., Liu W., Logan O., Lu J., Ly T.,
RA Martinez C., Oswal G., Perez L., Rashid N.D., Rowland K., Savage L.,
RA Scherer S.E., Shen H., Simon M., Stovall K., Timms K.M., Todd J.,
RA Vo O., Williamson A., Worley K.C., Yu W., Chinault C., Nelson D.,
RA Gibbs R.A.;
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
CC -!- TISSUE SPECIFICITY: Expressed only in testis.
CC -!- SIMILARITY: Contains 1 MAGE domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC
CC EMBL; X82539; CAA57889.1; -.
CC EMBL; S80936; AAC97145.1; -.
CC EMBL; AC005185; AAD10634.1; -.
CC Genew; HGNC:8608; MAGEB1.
CC H-invDB; HIX0016714; -.
CC MIN; 300097; -.

```

```
DR InterPro; IPR002190; MAGE.
DR Pfam; PF01454; MAGE; 1.
DR PROSITE; PS50838; MAGE; 1.
KW Antigen; Multigene family.
FT DOMAIN 108 307
FT CONFLICT 28 28
FT CONFLICT 172 172
FT CONFLICT 327 327
SQ SEQUENCE 347 AA; 39037 MW; 538A65E02DC34155 CRC64;

Query Match 76.5%; Score 39; DB 1; Length 347;
Best Local Similarity 77.8%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GLYDGMHHL 9
Db 228 GAYDGEHL 236

RESULT 9
ID Q96CWB PRELIMINARY; PRT; 347 AA.
AC Q96CWB;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Melanoma antigen, family B, 1.
GN Name=MAGEB1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinstead J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013772; AAH13772.1; -.
DR InterPro; IPR002190; MAGE.
DR Pfam; PF01454; MAGE; 1.
DR PROSITE; PS50838; MAGE; 1.
SQ SEQUENCE 347 AA; 39192 MW; C5F12C814EFC88E CRC64;

Query Match 76.5%; Score 39; DB 2; Length 347;
Best Local Similarity 77.8%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GLYDGMHHL 9
Db 228 GAYDGEHL 236

RESULT 9
ID Q96CWB PRELIMINARY; PRT; 347 AA.
AC Q96CWB;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Melanoma antigen, family B, 1.
GN Name=MAGEB1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinstead J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013772; AAH13772.1; -.
DR InterPro; IPR002190; MAGE.
DR Pfam; PF01454; MAGE; 1.
DR PROSITE; PS50838; MAGE; 1.
SQ SEQUENCE 347 AA; 39192 MW; C5F12C814EFC88E CRC64;

Query Match 76.5%; Score 39; DB 2; Length 347;
Best Local Similarity 77.8%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GLYDGMHHL 9
Db 228 GAYDGEHL 236

RESULT 10
Q96TGI PRELIMINARY; PRT; 347 AA.
AC Q96TGI;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE MAGE-B1.
GN Name=MAGE-B1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98110575; PubMed=9441743; DOI=10.1006/geno.1997.5052;
RA Lurquin C., De Smet C., Brasseur F., Muscatelli F., Martelange V.,
RA De Plaen E., Brasseur R., Monaco A.P., Boon T.;
RT "Two members of the human MAGEB gene family located in Xp21.3 are
RT expressed in tumors of various histological origins.";
RL Genomics 46:397-408(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Lurquin C.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; U93163; AAC23616.1; -.
DR PIR; I38008; I38008.
DR InterPro; IPR002190; MAGE.
DR Pfam; PF01454; MAGE; 1.
DR PROSITE; PS50838; MAGE; 1.
SQ SEQUENCE 347 AA; 39152 MW; 8C54E7ED80C739C0 CRC64;

Query Match 76.5%; Score 39; DB 2; Length 347;
Best Local Similarity 77.8%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GLYDGMHHL 9
Db 228 GAYDGEHL 236

RESULT 11
Q6FHJ0 PRELIMINARY; PRT; 347 AA.
AC Q6FHJ0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE MAGEB1 protein.
GN Name=MAGEB1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Halleck A., Ebert L., Mkomdinya M., Schick M., Eisenstein S.,
RA Neubert P., Kstrang K., Schatten R., Shen B., Henze S., Mar W.,
RA Korn B., Zuo D., Hu Y., LaBaer J.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR541762; CAG46562.1; -.
DR InterPro; IPR002190; MAGE.
DR Pfam; PF01454; MAGE; 1.
DR PROSITE; PS50838; MAGE; 1.
SQ SEQUENCE 347 AA; 39038 MW; 925E7DB4F19BD25D CRC64;

Query Match 76.5%; Score 39; DB 2; Length 347;
Best Local Similarity 77.8%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```

QY 1 GLYDGMHL 9
  ||| |||
  228 GAYDGEHL 236

RESULT 12
Q9TTY4 PRELIMINARY; PRT; 378 AA.
AC Q9TTY4;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Melanoma antigen.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=breed beagle; TISSUE=Testis;
RX MEDLINE=20470598; PubMed=11019919;
RA Ma Z., Khatlani T.S., Ohno K., Sasaki K., Inokuma H., Onishi T.;
RT "Cloning and sequencing of canine MAGE cDNA.";
RL Tissue Antigens 56:166-169(2000).
DR EMBL; AF187325; AAF01438.1; -.
DR InterPro; IPR002190; MAGE.
DR Pfam; PF01454; MAGE; 1.
DR PROSITE; PS0838; MAGE; 1.
DR SEQUENCE 378 AA; 42214 MW; AD09C6DC8E3C8D57 CRC64;

Query Match 76.5%; Score 39; DB 2; Length 378;
Best Local Similarity 87.5%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLYDGMHL 8
  ||| |||
  228 GLYAGMEH 235

RESULT 13
Q8DGG0 PRELIMINARY; PRT; 387 AA.
AC Q8DGG0;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Aspartate aminotransferase.
GN Name=aspC; OrderedLocNames=t12357;
OS Synechococcus elongatus (Thermosynechococcus elongatus).
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OX NCBI_TaxID=32046;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BP-1;
RX MEDLINE=2225144; PubMed=12240834;
RA Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S.,
RA Watanabe A., Iriyuchi M., Kawashima K., Kimura T., Kishida Y.,
RA Kiyokawa C., Kohara M., Matsunoto M., Matsuno A., Nakazaki N.,
RA Shimp S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the thermophilic cyanobacterium
Thermosynechococcus elongatus BP-1.";
RL DNA Res. 9:123-130(2002).
DR EMBL; AP005377; BAC09909.1; -.
DR HSSP; Q8RR70; 1J22.
DR GO; GO:0016847; F:i-aminocyclopropane-1-carboxylate synthase . . .; IEA.
DR GO; GO:0008483; F:transaminase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0009058; F:biosynthesis; IEA.
DR InterPro; IPR001176; ACC synthase.
DR InterPro; IPR004839; Aminotrans I/II.
DR InterPro; IPR004838; Nhrtransf_1_BS.
DR Pfam; PF00155; Aminotran 1.2; 1.
DR PRINTS; PR00753; ACCSYNTHASE.

QY 1 GLYDGMHL 9
  ||| |||
  209 LYDGAHL 216

RESULT 14
AAT_SYNY3 STANDARD; PRT; 389 AA.
AC Q55128;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Aspartate aminotransferase (EC 2.6.1.1) (Transaminase A) (ASPART).
GN Name=aspC; OrderedLocNames=s110402;
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96127525; PubMed=8590279;
RA Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
RA Sugiura M., Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
region from map positions 64k to 92k of the genome.";
RL DNA Res. 2:153-166(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hiroseawa M., Sugiura M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
RA Shimp S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
Synechocystis sp. strain PCC6803. II. Sequence determination of the
entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
CC -1- CARBONIC ACTIVITY: L-aspartate + 2-oxoglutarate = oxaloacetate +
L-glutamate.
CC -1- COFACTOR: Pyridoxal phosphate (By similarity).
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the class-I pyridoxal-phosphate-dependent
aminotransferase family.
-----
This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
-----
EMBL; D64001; BAA10261.1; -.
PIR; S74343; S74343.
HSSP; Q8RR70; 1J32.
DR InterPro; IPR001176; ACC synthase.
DR InterPro; IPR004839; Aminotrans I/II.
DR InterPro; IPR004838; Nhrtransf_1_BS.
DR Pfam; PF00155; Aminotran 1.2; 1.
DR PRINTS; PR00753; ACCSYNTHASE.
DR PROSITE; PS00105; AA-TRANSFER CLASS_1; 1.
KW Aminotransferase; Complete proteome; Pyridoxal phosphate; Transferase.
AMINOTRANSFERASE; Complete proteome; Pyridoxal phosphate (By similarity).
BINDING 238 238

```


SQ SEQUENCE 389 AA; 42352 MW; 7706C9C353EA317F CRC64;

Query Match 76.5%; Score 39; DB 1; Length 389;
 Best Local Similarity 87.5%; Pred. No. 78;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LYDGMHL 9

|||||

Db 210 LYDGMHL 217

RESULT 15

Q94EG1
 ID Q94EG1 PRELIMINARY; PRT; 394 AA.
 AC Q94EG1;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Putative aspartate transaminase.
 GN Name=P0509B06.2;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RZ SEQUENCE FROM N.A.
 RX PubMed=12447438; DOI=10.1038/nature01184;
 RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
 Wu J., Nilmura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
 RA Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,
 RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
 RA Hijishita S., Honda M., Ichikawa Y., Igouna A., Iijima M., Ikeda M.,
 RA Ikeno M., Itoh T., Itoh Y., Iwabuchi A., Kamiya K.,
 RA Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
 RA Machita K., Maehara T., Mizuno H., Mizubayashi I., Mukai Y.,
 RA Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
 RA Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai K., Shibata M.,
 RA Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,
 RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
 RA Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,
 RA Yano M., Jiang J., Gojobori T.;
 RT "The genome sequence and structure of rice chromosome 1."
 RL Nature 420:312-316(2002).
 DR EMBL; AP002903; BAB63467.1; -.
 DR HSSP; Q56232; 5B34.
 DR Gramene; Q94EG1; -.
 DR GO; GO:0008483; F:transaminase activity; IEA.
 DR GO; GO:0009058; P:biosynthesis; IEA.
 DR InterPro; IPR004839; AminoTrans I/II.
 DR InterPro; IPR004838; NHtransf 1_BS.
 DR Pfam; PF00155; AminoTran 1_2_1.
 DR PROSITE; PS00105; AX_TRANSFER_CLASS_1; 1.
 SQ SEQUENCE 394 AA; 43747 MW; 8E843B36D6D2762 CRC64;

Query Match 76.5%; Score 39; DB 2; Length 394;
 Best Local Similarity 85.7%; Pred. No. 79;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LYDGMHL 8

|||||

Db 211 MYDGMHL 217

Search completed: November 15, 2005, 15:43:48
 Job time : 7.2619 secs

THIS PAGE BLANK (USPTO)

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 15, 2005, 15:33:16 ; Search time 1.45238 Seconds
(without alignments)
462.579 Million cell updates/sec

Title: US-09-856-812B-42
Sequence: 1 GLYDGMHL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/protdata/1/iaa/5A COMB.pep.*
2: /cgn2_6/protdata/1/iaa/5B COMB.pep.*
3: /cgn2_6/protdata/1/iaa/6A COMB.pep.*
4: /cgn2_6/protdata/1/iaa/6B COMB.pep.*
5: /cgn2_6/protdata/1/iaa/PCTUS COMB.pep.*
6: /cgn2_6/protdata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	51	100.0	369	2	US-08-773-870-4
2	40	78.4	398	2	US-08-599-171A-29
3	40	78.4	398	2	US-08-646-590B-29
4	40	78.4	398	3	US-09-069-226-29
5	40	78.4	398	3	US-09-412-184-29
6	39	76.5	249	4	US-09-248-796A-22159
7	39	76.5	347	2	US-08-773-870-3
8	39	76.5	397	4	US-09-949-016-11171
9	39	76.5	397	4	US-09-949-016-11172
10	39	76.5	494	4	US-09-252-991A-28162
11	38	74.5	10	4	US-09-165-863-44
12	38	74.5	10	4	US-09-289-350-44
13	38	74.5	10	4	US-09-806-769-44
14	38	74.5	312	4	US-09-949-016-9310
15	36	70.6	237	2	US-08-970-133-5
16	36	70.6	237	3	US-09-294-545-5
17	35	68.6	94	4	US-09-732-210-1213
18	35	68.6	180	1	US-08-049-473-31
19	35	68.6	180	1	US-08-312-648-31
20	35	68.6	180	5	PCT-US94-04190-31
21	35	68.6	192	4	US-09-949-016-9891
22	35	68.6	212	4	US-09-710-279-642
23	35	68.6	217	4	US-09-710-279-2556
24	35	68.6	311	3	US-09-308-003-52
25	35	68.6	333	4	US-09-710-279-2890
26	35	68.6	341	3	US-09-134-001C-3497
27	35	68.6	347	3	US-09-134-001C-2986

28	35	68.6	493	4	US-09-328-352-6663	Sequence 6663, Ap
29	34	66.7	63	4	US-09-107-532A-6771	Sequence 6771, Ap
30	34	66.7	181	1	US-08-418-44A-7	Sequence 7, Appl
31	34	66.7	185	4	US-09-248-796A-20264	Sequence 20264, A
32	34	66.7	333	3	US-08-938-546-2	Sequence 2, Appl
33	34	66.7	333	3	US-09-340-812-2	Sequence 2, Appl
34	34	66.7	339	3	US-08-938-546-4	Sequence 4, Appl
35	34	66.7	339	3	US-09-340-812-4	Sequence 4, Appl
36	34	66.7	341	3	US-09-134-001C-4268	Sequence 4268, Ap
37	34	66.7	489	4	US-09-540-236-3571	Sequence 3571, Ap
38	34	66.7	742	4	US-09-107-532A-4996	Sequence 4996, Ap
39	34	66.7	909	3	US-08-936-135-8	Sequence 8, Appl
40	34	66.7	909	3	US-08-936-135-10	Sequence 10, Appl
41	34	66.7	909	3	US-08-936-135-18	Sequence 18, Appl
42	34	66.7	909	4	US-09-439-711C-8	Sequence 8, Appl
43	34	66.7	909	4	US-09-439-711C-10	Sequence 10, Appl
44	34	66.7	909	4	US-09-439-711C-18	Sequence 18, Appl
45	34	66.7	914	3	US-08-936-135-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-08-773-870-4
; Sequence 4, Application US/08773870
; Patent No. 5912143
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL HUMAN MAGE-LIKE PROTEIN
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESS: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/773,870
; FILING DATE: Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0179 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 369 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 533511
; US-08-773-870-4

Query Match 100.0%; Score 51; DB 2; Length 369;
Best Local Similarity 100.0%; Pred. NO. 0.092;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLYDGMHL 9
Db 254 GLYDGMHL 262

RESULT 2
US-08-599-171A-29
; Sequence 29, Application US/08599171A
; Patent No. 5814473
; GENERAL INFORMATION:
; APPLICANT: WARREN, Patrick V.
; TITLE OF INVENTION: TRANSAMINASES AND AMINOTRANSFERASES
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/599,171A
; FILING DATE: Concurrently
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Ph.D., Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 09010/017001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 398 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-646-590B-29

Query Match 78.4%; Score 40; DB 2; Length 398;
Best Local Similarity 75.0%; Pred. No. 12;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LYDGMHL 9
Db 210 IYDGMHL 217

RESULT 4
US-09-069-226-29
; Sequence 29, Application US/09069226
; Patent No. 6013509
; GENERAL INFORMATION:
; APPLICANT: WARREN, Patrick V.
; TITLE OF INVENTION: TRANSAMINASES AND AMINOTRANSFERASES
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/069,226
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/599,171
; FILING DATE: 09-FEB-1996
; PRIOR APPLICATION DATA: PCT/US97/01094
; FILING DATE: 21-January-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Ph.D., Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 09010/017001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 398 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-646-590B-29

Query Match 78.4%; Score 40; DB 2; Length 398;
Best Local Similarity 75.0%; Pred. No. 12;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LYDGMHL 9
Db 210 IYDGMHL 217

RESULT 3
US-08-646-590B-29
; Sequence 29, Application US/08646590B
; Patent No. 5962283
; GENERAL INFORMATION:
; APPLICANT: Warren, Patrick V.
; APPLICANT: Swanson, Ronald V.
; TITLE OF INVENTION: TRANSAMINASES AND AMINOTRANSFERASES
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA

REGISTRATION NUMBER: 28,019
REFERENCE/DOCKET NUMBER: 331400-38
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 398 AMINO ACIDS
TYPE: AMINO ACID
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
US-09-069-226-29

Query Match 78.4%; Score 40; DB 3; Length 398;
Best Local Similarity 75.0%; Pred. No. 12;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LYDGMHL 9
Db 210 IYDGMHV 217

RESULT 5

US-09-412-184-29
Sequence 29, Application US/09412184
Patent No. 6268188

GENERAL INFORMATION:

APPLICANT: Warren, Patrick V.
APPLICANT: Swanson, Ronald V.
TITLE OF INVENTION: TRANSAMINASES AND AMINOTRANSFERASES
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: US

ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/412,184
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/646,590
FILING DATE: 08-May-1996
APPLICATION NUMBER: 08/599,171
FILING DATE: 09-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/01094
FILING DATE: 21-January-1997

CLASSIFICATION:

NAME: Haile, Ph.D., Lies A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 09010/017001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099

INFORMATION FOR SEQ ID NO: 29:

SEQUENCE CHARACTERISTICS:
LENGTH: 398 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-09-412-184-29

Query Match 78.4%; Score 40; DB 3; Length 398;

Best Local Similarity 75.0%; Pred. No. 12;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 2 LYDGMHL 9
Db 210 IYDGMHV 217

RESULT 6

US-09-248-796A-22159
Sequence 22159, Application US/09248796A
Patent No. 6747137

GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 22159
TYPE: PRT
LENGTH: 249

ORGANISM: Candida albicans

US-09-248-796A-22159

Query Match 76.5%; Score 39; DB 4; Length 249;
Best Local Similarity 75.0%; Pred. No. 11;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLYDGMHL 8
Db 31 GLYDGLNH 38

RESULT 7

US-08-773-870-3
Sequence 3, Application US/08773870
Patent No. 5912143

GENERAL INFORMATION:

APPLICANT: Bandman, Olga
APPLICANT: Goli, Suvya K.
TITLE OF INVENTION: NOVEL HUMAN MAGE-LIKE PROTEIN
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/773,870

FILING DATE: Herewith

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0179 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-0555

```
; TELFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 347 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 608993
US-08-773-870-3

Query Match          76.5%; Score 39; DB 2; Length 347;
Best Local Similarity 77.8%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GLYDGMHHL 9
Db 228 GAYDGEHL 236

RESULT 8
US-09-949-016-11171
; Sequence 11171, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11171
; LENGTH: 397
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11171

Query Match          76.5%; Score 39; DB 4; Length 397;
Best Local Similarity 77.8%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GLYDGMHHL 9
Db 278 GAYDGEHL 286

RESULT 9
US-09-949-016-11172
; Sequence 11172, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
```

```
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11172
; LENGTH: 397
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11172

Query Match          76.5%; Score 39; DB 4; Length 397;
Best Local Similarity 77.8%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GLYDGMHHL 9
Db 278 GAYDGEHL 286

RESULT 10
US-09-252-991A-28162
; Sequence 28162, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 28162
; LENGTH: 494
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28162

Query Match          76.5%; Score 39; DB 4; Length 494;
Best Local Similarity 77.8%; Pred. No. 23;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLYDGMHHL 9
Db 302 GLADGLEHL 310

RESULT 11
US-09-165-863-44
; Sequence 44, Application US/09165863
; Patent No. 6407063
; GENERAL INFORMATION:
; APPLICANT: Luiten, Rosalie
; APPLICANT: Duffour, Marie-Therese
; APPLICANT: Demotte, Nathalie
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Cornelis, Guy
; APPLICANT: Stroobant, Vincent
; APPLICANT: Lurquin, Christophe
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: Chauv, Pascal
; TITLE OF INVENTION: TUMOR ANTIGENS AND CTL CLONES ISOLATED BY A NOVEL
; PROCEDURE
; FILE REFERENCE: 11727
; CURRENT APPLICATION NUMBER: US/09/165,863
; CURRENT FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human MAGE-A4 peptide
```

US-09-165-863-44

Query Match 74.5%; Score 38; DB 4; Length 10;
Best Local Similarity 75.0%; Pred. No. 0.49;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLYDGMH 8
Db 1 GYDGRH 8

RESULT 12

US-09-289-350-44
Sequence 44, Application US/09289350

Patent No. 6531451

GENERAL INFORMATION:

APPLICANT: Chau, Pascal

APPLICANT: Luiten, Rosalie

APPLICANT: Demotte, Nathalie

APPLICANT: Delfour, Marie-Therese

APPLICANT: Lurquin, Christophe

APPLICANT: Traversari, Catia

APPLICANT: Stroobant, Vincent

APPLICANT: Cornelis, Guy R.

APPLICANT: Boon-Falleur, Thierry

APPLICANT: Van Der Bruggen, Pierre

TITLE OF INVENTION: TUMOR ANTIGENS AND CTL CLONES ISOLATED BY A NOVEL

FILE REFERENCE: 117272

CURRENT APPLICATION NUMBER: US/09/289,350

CURRENT FILING DATE: 1999-04-09

PRIOR APPLICATION NUMBER: 09/165,863

PRIOR FILING DATE: 1998-10-02

NUMBER OF SEQ ID NOS: 49

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 44

LENGTH: 10

TYPE: PRT

ORGANISM: Human MAGE-A4 peptide

US-09-289-350-44

Query Match 74.5%; Score 38; DB 4; Length 10;
Best Local Similarity 75.0%; Pred. No. 0.49;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLYDGMH 8
Db 1 GYDGRH 8

RESULT 13

US-09-806-769-44

Sequence 44, Application US/09806769

Patent No. 6710172

GENERAL INFORMATION:

APPLICANT: Chau, Pascal

APPLICANT: Luiten, Rosalie

APPLICANT: Demotte, Nathalie

APPLICANT: Delfour, Marie-Therese

APPLICANT: Lurquin, Christophe

APPLICANT: Traversari, Catia

APPLICANT: Stroobant, Vincent

APPLICANT: Cornelis, Guy R.

APPLICANT: Boon-Falleur, Thierry

APPLICANT: Van Der Bruggen, Pierre

APPLICANT: Schults, Erwin

APPLICANT: Warnier, Guy

TITLE OF INVENTION: TUMOR ANTIGENS AND CTL CLONES ISOLATED BY A NOVEL

FILE REFERENCE: 117272y

CURRENT APPLICATION NUMBER: US/09/806,769

CURRENT FILING DATE: 2001-04-03

PRIOR APPLICATION NUMBER: 09/165,863

PRIOR FILING DATE: 1998-10-02
PRIOR APPLICATION NUMBER: 09/289,350
PRIOR FILING DATE: 1999-04-09
PRIOR APPLICATION NUMBER: 09/806,769
PRIOR FILING DATE: 2001-04-02
NUMBER OF SEQ ID NOS: 57
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 44
LENGTH: 10
TYPE: PRT
ORGANISM: Human MAGE-A4 peptide
US-09-806-769-44

Query Match 74.5%; Score 38; DB 4; Length 10;
Best Local Similarity 75.0%; Pred. No. 0.49;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLYDGMH 8
Db 1 GYDGRH 8

RESULT 14

US-09-949-016-9310

Sequence 9310, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 9310

LENGTH: 312

TYPE: PRT

ORGANISM: Human

US-09-949-016-9310

Query Match 74.5%; Score 38; DB 4; Length 312;
Best Local Similarity 66.7%; Pred. No. 21;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GLYDGMH 9
Db 194 GYDGRHL 202

RESULT 15

US-08-970-133-5

Sequence 5, Application US/08970133

Patent No. 5916753

GENERAL INFORMATION:

APPLICANT: Bandman, Olga

APPLICANT: Guegler, Karl J.

APPLICANT: Lal, Preeti

TITLE OF INVENTION: SH3-CONTAINING PROTEINS

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Dr.

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

```
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/970,133
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0419 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 237 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1255033
US-08-970-133-5

Query Match      70.6%; Score 36; DB 2; Length 237;
Best Local Similarity 75.0%; Pred. No. 38;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GLYDGMH 8
Db      114 GLYDGMH 121

Search completed: November 15, 2005, 15:45:52
Job time : 1.45238 secs
```


GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 15, 2005, 15:35:58 ; Search time 5.35714 Seconds
(without alignments)
702.928 Million cell updates/sec

Title: US-09-856-812B-42
Perfect score: 51
Sequence: 1 GLYDGMHL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	51	100.0	9	10	US-09-865-548A-39
2	51	100.0	9	15	US-10-164-121A-13
3	51	100.0	9	15	US-10-164-078A-12
4	51	100.0	9	15	US-10-447-161-29
5	51	100.0	9	16	US-10-651-616-24
6	51	100.0	9	16	US-10-362-715-8
7	51	100.0	9	17	US-10-705-459-39
8	51	100.0	9	18	US-10-776-521B-392
9	51	100.0	9	18	US-10-941-150A-13
10	51	100.0	20	18	US-10-776-521B-398
11	51	100.0	20	18	US-10-820-067A-896

12	51	100.0	369	14	US-10-036-542-84	Sequence 84, Appl
13	51	100.0	369	15	US-10-188-832-149	Sequence 149, Appl
14	51	100.0	369	17	US-10-658-884-4	Sequence 4, Appl
15	51	100.0	369	18	US-10-756-149-4721	Sequence 4721, Ap
16	51	100.0	383	14	US-10-029-386-32058	Sequence 32058, A
17	43	84.3	347	15	US-10-094-749-3202	Sequence 3202, Ap
18	40	78.4	398	9	US-09-905-173-29	Sequence 29, Appl
19	40	78.4	398	14	US-10-060-432-29	Sequence 29, Appl
20	40	78.4	419	15	US-10-369-493-2919	Sequence 2919, Ap
21	39	76.5	185	15	US-10-425-114-68250	Sequence 68250, A
22	39	76.5	134	16	US-10-425-115-304865	Sequence 304865
23	39	76.5	347	16	US-10-408-765A-1695	Sequence 1695, Ap
24	39	76.5	347	17	US-10-658-884-3	Sequence 3, Appl
25	39	76.5	372	15	US-10-425-114-53891	Sequence 53891, A
26	39	76.5	383	15	US-10-425-114-59141	Sequence 59141, A
27	39	76.5	389	15	US-10-369-493-2802	Sequence 2802, Ap
28	39	76.5	395	16	US-10-425-115-304870	Sequence 304870, Ap
29	39	76.5	415	16	US-10-437-963-173687	Sequence 173687, Ap
30	38	74.5	10	10	US-09-865-548A-38	Sequence 38, Appl
31	38	74.5	10	15	US-10-164-121A-18	Sequence 18, Appl
32	38	74.5	10	15	US-10-164-078A-17	Sequence 17, Appl
33	38	74.5	10	15	US-10-447-161-27	Sequence 27, Appl
34	38	74.5	10	15	US-10-218-095-10	Sequence 10, Appl
35	38	74.5	10	16	US-10-753-158-44	Sequence 9, Appl
36	38	74.5	10	16	US-10-362-715-9	Sequence 44, Appl
37	38	74.5	10	17	US-10-705-459-38	Sequence 38, Appl
38	38	74.5	10	18	US-10-941-150A-18	Sequence 18, Appl
39	38	74.5	215	9	US-09-864-761-36170	Sequence 36170, A
40	38	74.5	317	14	US-10-157-031-52	Sequence 52, Appl
41	38	74.5	317	15	US-10-218-095-2	Sequence 2, Appl
42	38	74.5	317	17	US-10-482-029-148	Sequence 148, App
43	38	74.5	317	18	US-10-756-149-4740	Sequence 4740, Ap
44	37	72.5	10	10	US-09-865-548A-20	Sequence 20, Appl
45	37	72.5	10	17	US-10-705-459-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1
US-09-865-548A-39
; Sequence 39, Application US/09865548A
; Publication No. US20030096298A1
; GENERAL INFORMATION:
; APPLICANT: Barnea, Bilon
; APPLICANT: Beer, Ilan
; APPLICANT: Ziv, Tamar
; APPLICANT: Admon, Arie
; TITLE OF INVENTION: METHOD OF IDENTIFYING PEPTIDES CAPABLE OF BINDING TO MHC MOLECULES
; TITLE OF INVENTION: PEPTIDES IDENTIFIED THEREBY AND THEIR USES
; FILE REFERENCE: 01/22080
; CURRENT APPLICATION NUMBER: US/09/865,548A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: US 60/290,958
; PRIOR FILING DATE: 2001-05-16
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-865-548A-39

Query Match 100.0%; Score 51; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLYDGMHL 9

Db 1 GLYDGMHL 9

```
RESULT 2
US-10-164-121A-13
; Sequence 13, Application US/10164121A
; Publication No. US20030228308A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Yi
; APPLICANT: Boon, Thierry
; APPLICANT: Van der Bruggen, Pierre
; APPLICANT: Traversari, Catra
; TITLE OF INVENTION: Isolated Peptides Which Bind to HLA-Cw6 Molecules And Uses Thereof
; FILE REFERENCE: LUD-5771
; CURRENT APPLICATION NUMBER: US/10/164,121A
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 36
; SEQ ID NO 13
; LENGTH: 9
; TYPE: PRT
; ORGANISM: H. sapiens
; FEATURE:
US-10-164-121A-13

Query Match      100.0%; Score 51; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GLYDGMHGL 9
Db      1 GLYDGMHGL 9

RESULT 3
US-10-164-078A-12
; Sequence 12, Application US/10164078A
; Publication No. US20030228325A1
; GENERAL INFORMATION:
; APPLICANT: Bilsborough, Janine
; APPLICANT: Schultz, Erwin
; APPLICANT: Panichelli, Christophe
; APPLICANT: Van der Bruggen, Pierre
; APPLICANT: Boon, Thierry
; TITLE OF INVENTION: Isolated Peptides Which Bind to HLA-B18 Molecules And Uses Thereof
; FILE REFERENCE: LUD-5756
; CURRENT APPLICATION NUMBER: US/10/164,078A
; CURRENT FILING DATE: 2002-06-05
; NUMBER OF SEQ ID NOS: 35
; SEQ ID NO 12
; LENGTH: 9
; TYPE: PRT
; ORGANISM: H. sapiens
; FEATURE:
US-10-164-078A-12

Query Match      100.0%; Score 51; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GLYDGMHGL 9
Db      1 GLYDGMHGL 9

RESULT 4
US-10-447-161-29
; Sequence 29, Application US/10447161
; Publication No. US20040023314A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Rong-fu
; TITLE OF INVENTION: Mutant Fibronectin and Tumor Metastasis
; FILE REFERENCE: HO-P02484US1
; CURRENT APPLICATION NUMBER: US/10/447,161
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/383,530
```

```
; PRIOR FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-447-161-29

Query Match      100.0%; Score 51; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GLYDGMHGL 9
Db      1 GLYDGMHGL 9

RESULT 5
US-10-651-616-24
; Sequence 24, Application US/10651616
; Publication No. US20040253235A1
; GENERAL INFORMATION:
; APPLICANT: CytoCure, LLC
; APPLICANT: DURDA, PAUL
; TITLE OF INVENTION: METHODS FOR UP-REGULATING ANTIGEN EXPRESSION IN TUMORS
; FILE REFERENCE: 027823-0305578
; CURRENT APPLICATION NUMBER: US/10/651,616
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: 60/407,492
; PRIOR FILING DATE: 2002-08-29
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Homo sapien artificial
US-10-651-616-24

Query Match      100.0%; Score 51; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GLYDGMHGL 9
Db      1 GLYDGMHGL 9

RESULT 6
US-10-362-715-8
; Sequence 8, Application US/10362715
; Publication No. US20040253574A1
; GENERAL INFORMATION:
; APPLICANT: Schuler, Gerold
; APPLICANT: Schuler-Thurner, Beatrice
; TITLE OF INVENTION: METHOD FOR READY-TO-USE, ANTIGEN LOADED OR UNLOADED,
; FILE REFERENCE: 1430/12
; CURRENT APPLICATION NUMBER: US/10/362,715
; CURRENT FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-362-715-8
```

```
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heat shock protein binding domain
US-10-776-521B-392

Query Match      100.0%; Score 51; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLYDGMHEHL 9
   |||||
Db 1 GLYDGMHEHL 9

RESULT 7
US-10-705-459-39
; Sequence 39, Application US/10705459
; Publication No. US20050053918A1
; GENERAL INFORMATION:
; APPLICANT: Barnea, Eilon
; APPLICANT: Beer, Ilan
; APPLICANT: Ziv, Tamar
; APPLICANT: Admon, Arie
; APPLICANT: Dassa, Lior
; APPLICANT: Buchsbaum, Samuel
; TITLE OF INVENTION: METHOD OF IDENTIFYING PEPTIDES CAPABLE OF BINDING TO MHC MOLECULES
; TITLE OF INVENTION: PEPTIDES IDENTIFIED THEREBY AND THEIR USES
; FILE REFERENCE: 26884
; CURRENT APPLICATION NUMBER: US/10/705.459
; CURRENT FILING DATE: 2003-11-12
; NUMBER OF SEQ ID NOS: 372
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-705-459-39

Query Match      100.0%; Score 51; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLYDGMHEHL 9
   |||||
Db 1 GLYDGMHEHL 9

RESULT 8
US-10-776-521B-392
; Sequence 392, Application US/10776521B
; Publication No. US20050202033A1
; GENERAL INFORMATION:
; APPLICANT: Fletcher, Jessica
; APPLICANT: Prince-Cohane, Kenya
; APPLICANT: Mehta, Sunil
; APPLICANT: Slusarewicz, Paul
; APPLICANT: Andjelic, Sofija
; APPLICANT: Barber, Brian
; TITLE OF INVENTION: IMPROVED HEAT SHOCK PROTEIN-BASED VACCINES AND
; TITLE OF INVENTION: IMMUNOTHERAPIES
; FILE REFERENCE: 8449-405-999
; CURRENT APPLICATION NUMBER: US/10/776.521B
; CURRENT FILING DATE: 2004-02-12
; PRIOR APPLICATION NUMBER: 60/503,417
; PRIOR FILING DATE: 2003-09-16
; PRIOR FILING DATE: 2003-09-16
; PRIOR FILING DATE: 2003-04-18
; PRIOR FILING DATE: 2003-04-11
; PRIOR FILING DATE: 2003-04-11
; PRIOR FILING DATE: 2003-02-13
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 392
; LENGTH: 9
```

```
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heat shock protein binding domain
US-10-776-521B-392

Query Match      100.0%; Score 51; DB 18; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLYDGMHEHL 9
   |||||
Db 1 GLYDGMHEHL 9

RESULT 9
US-10-941-150A-13
; Sequence 13, Application US/10941150A
; Publication No. US20050226881A1
; GENERAL INFORMATION:
; APPLICANT: VAN DER BRUGGEN, Pierre
; APPLICANT: BOON-PALLEUR, Thierry
; APPLICANT: BRECKPOT, Karine
; APPLICANT: THIELEMANS, Kris
; TITLE OF INVENTION: ISOLATED PEPTIDE WHICH BINDS TO HLA-CW*07 AND USES THEREOF
; FILE REFERENCE: LUD-5853-US (10411307)
; CURRENT APPLICATION NUMBER: US/10/941.150A
; CURRENT FILING DATE: 2004-09-15
; PRIOR APPLICATION NUMBER: US 60/504,874
; PRIOR FILING DATE: 2003-09-22
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Derived from MAGEA10
US-10-941-150A-13

Query Match      100.0%; Score 51; DB 18; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLYDGMHEHL 9
   |||||
Db 1 GLYDGMHEHL 9

RESULT 10
US-10-776-521B-398
; Sequence 398, Application US/10776521B
; Publication No. US20050202033A1
; GENERAL INFORMATION:
; APPLICANT: Fletcher, Jessica
; APPLICANT: Prince-Cohane, Kenya
; APPLICANT: Mehta, Sunil
; APPLICANT: Slusarewicz, Paul
; APPLICANT: Andjelic, Sofija
; APPLICANT: Barber, Brian
; TITLE OF INVENTION: IMPROVED HEAT SHOCK PROTEIN-BASED VACCINES AND
; TITLE OF INVENTION: IMMUNOTHERAPIES
; FILE REFERENCE: 8449-405-999
; CURRENT APPLICATION NUMBER: US/10/776.521B
; CURRENT FILING DATE: 2004-02-12
; PRIOR APPLICATION NUMBER: 60/503,417
; PRIOR FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: 60/463,746
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: 60/462,469
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 60/447,142
; PRIOR FILING DATE: 2003-02-13
```

; NUMBER OF SEQ ID NOS: 419
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 398
 ; LENGTH: 20
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Hybrid antigen
 US-10-776-521B-398

Query Match 100.0%; Score 51; DB 18; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.018;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLYDGMHL 9
 |||||
 Db 1 GLYDGMHL 9

RESULT 11

US-10-820-067A-896

; Sequence 896, Application US/10820067A
 ; Publication No. US20050214312A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Fletcher, J.
 ; APPLICANT: Prince-Cohane, K.
 ; APPLICANT: Mehta, S.
 ; APPLICANT: Slusarewicz, P.
 ; APPLICANT: Andjelic, S.
 ; APPLICANT: Barber, B.
 ; TITLE OF INVENTION: IMPROVED HEAT SHOCK PROTEIN-BASED
 ; FILE REFERENCE: 8449-406-999
 ; CURRENT APPLICATION NUMBER: US/10/820,067A
 ; CURRENT FILING DATE: 2004-04-08
 ; PRIOR APPLICATION NUMBER: 60/462,469
 ; PRIOR FILING DATE: 2003-04-11
 ; PRIOR APPLICATION NUMBER: 60/463,746
 ; PRIOR FILING DATE: 2003-04-18
 ; PRIOR APPLICATION NUMBER: 60/503,417
 ; PRIOR FILING DATE: 2003-09-16
 ; NUMBER OF SEQ ID NOS: 926
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 896
 ; LENGTH: 20
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Hybrid antigen
 US-10-820-067A-896

Query Match 100.0%; Score 51; DB 18; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.018;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLYDGMHL 9
 |||||
 Db 1 GLYDGMHL 9

RESULT 12

US-10-036-542-84
 ; Sequence 84, Application US/10036542
 ; Publication No. US20030083481A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Birse et al.
 ; TITLE OF INVENTION: 25 Human Prostate and Prostate Cancer Associated Proteins
 ; FILE REFERENCE: PA002P1
 ; CURRENT APPLICATION NUMBER: US/10/036,542
 ; CURRENT FILING DATE: 2002-01-07
 ; PRIOR APPLICATION NUMBER: PCT/US00/19666
 ; PRIOR FILING DATE: 2000-07-20
 ; PRIOR APPLICATION NUMBER: 60/144,972

; PRIOR FILING DATE: 1999-07-21
 ; PRIOR APPLICATION NUMBER: 60/148,681
 ; PRIOR FILING DATE: 1999-08-13
 ; PRIOR APPLICATION NUMBER: 60/149,173
 ; PRIOR FILING DATE: 1999-08-17
 ; PRIOR APPLICATION NUMBER: 60/158,004
 ; PRIOR FILING DATE: 1999-10-06
 ; PRIOR APPLICATION NUMBER: 60/194,689
 ; PRIOR FILING DATE: 2000-04-05
 ; NUMBER OF SEQ ID NOS: 157
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 84
 ; LENGTH: 369
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-036-542-84

Query Match 100.0%; Score 51; DB 14; Length 369;
 Best Local Similarity 100.0%; Pred. No. 0.41;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLYDGMHL 9
 |||||
 Db 254 GLYDGMHL 262

RESULT 13

US-10-188-832-149
 ; Sequence 149, Application US/10188832
 ; Publication No. US20040076955A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mack, David H.
 ; APPLICANT: Aziz, Natasha
 ; TITLE OF INVENTION: Methods of Diagnosis of Bladder Cancer, Compositions
 ; TITLE OF INVENTION: and Methods of Screening for Modulators of Bladder
 ; FILE REFERENCE: 018501-002330US
 ; CURRENT APPLICATION NUMBER: US/10/188,832
 ; CURRENT FILING DATE: 2002-11-22
 ; PRIOR APPLICATION NUMBER: US 60/302,814
 ; PRIOR FILING DATE: 2001-07-03
 ; PRIOR APPLICATION NUMBER: US 60/310,099
 ; PRIOR FILING DATE: 2001-08-03
 ; PRIOR APPLICATION NUMBER: US 60/343,705
 ; PRIOR FILING DATE: 2001-11-08
 ; PRIOR APPLICATION NUMBER: US 60/350,666
 ; PRIOR FILING DATE: 2001-11-13
 ; PRIOR APPLICATION NUMBER: US 60/372,246
 ; PRIOR FILING DATE: 2002-04-12
 ; NUMBER OF SEQ ID NOS: 207
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 149
 ; LENGTH: 369
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-188-832-149

Query Match 100.0%; Score 51; DB 15; Length 369;
 Best Local Similarity 100.0%; Pred. No. 0.41;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLYDGMHL 9
 |||||
 Db 254 GLYDGMHL 262

RESULT 14

US-10-658-884-4
 ; Sequence 4, Application US/10658884
 ; Publication No. US20050019304A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bandman, Olga

Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN MAGE-LIKE PROTEIN
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/658,884
FILING DATE: 09-Sep-2003
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/773,870
FILING DATE: 27-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0179 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 369 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 533511
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-658-884-4

Query Match 100.0%; Score 51; DB 17; Length 369;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLYDGMHL 9
Db 254 GLYDGMHL 262

RESULT 15
US-10-756-149-4721
; Sequence 4721, Application US/10756149
; Publication No. US20050181375A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Zlotnick, Albert
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND
; TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
; FILE REFERENCE: file
; CURRENT APPLICATION NUMBER: US/10/756,149
; CURRENT FILING DATE: 2004-01-12
; NUMBER OF SEQ ID NOS: 5818
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 4721
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-756-149-4721

Query Match 100.0%; Score 51; DB 18; Length 369;
Best Local Similarity 100.0%; Pred. No. 0.41;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GLYDGMHL 9
Db 254 GLYDGMHL 262
Search completed: November 15, 2005, 15:49:49
Job time : 6.35714 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 15, 2005, 15:50:00 ; Search time 163 Seconds
(without alignments)
23.102 Million cell updates/sec

Title: US-09-856-812B-42

Perfect score: 51

Sequence: 1 GLYDGMHEHL 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 180914

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*
1: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	51	100.0	9	10	US-09-856-548A-39
2	51	100.0	9	15	US-10-149-138-2681
3	51	100.0	9	15	US-10-149-138-3329
4	51	100.0	9	15	US-10-149-138-3338
5	51	100.0	9	16	US-10-149-138-3335
6	51	100.0	9	16	US-10-149-138-3338
7	51	100.0	9	17	US-10-149-138-3335
8	51	100.0	9	18	US-10-149-138-3335
9	51	100.0	9	18	US-10-149-138-3338
10	28	54.9	8	15	US-10-149-138-3338
11	28	54.9	8	15	US-10-149-138-3335

12	28	54.9	8	15	US-10-149-138-2092
13	28	54.9	8	15	US-10-149-138-2681
14	28	54.9	8	15	US-10-149-138-3329
15	28	54.9	8	16	US-10-149-138-3338
16	28	54.9	8	16	US-10-149-138-901
17	28	54.9	8	16	US-10-149-138-2092
18	28	54.9	8	16	US-10-149-138-2681
19	28	54.9	8	16	US-10-149-138-3329
20	28	54.9	9	10	US-09-865-548A-155
21	28	54.9	9	15	US-10-149-138-905
22	28	54.9	9	15	US-10-149-138-1078
23	28	54.9	9	15	US-10-149-138-2689
24	28	54.9	9	15	US-10-149-138-3163
25	28	54.9	9	15	US-10-149-138-3335
26	28	54.9	9	15	US-10-149-138-3638
27	28	54.9	9	15	US-10-149-138-3658
28	28	54.9	9	15	US-10-149-138-3969
29	28	54.9	9	15	US-10-149-138-4144
30	28	54.9	9	16	US-10-149-138-905
31	28	54.9	9	16	US-10-149-138-1078
32	28	54.9	9	16	US-10-149-138-2689
33	28	54.9	9	16	US-10-149-138-3163
34	28	54.9	9	16	US-10-149-138-3335
35	28	54.9	9	16	US-10-149-138-3638
36	28	54.9	9	16	US-10-149-138-3658
37	28	54.9	9	16	US-10-149-138-3969
38	28	54.9	9	16	US-10-149-138-4144
39	28	54.9	9	17	US-10-705-459-155
40	27	52.9	9	18	US-10-999-364-4
41	26	51.0	8	14	US-10-273-541-41
42	24	47.1	6	16	US-10-699-088-896
43	24	47.1	6	16	US-10-699-113-896
44	24	47.1	6	17	US-10-699-114-896
45	24	47.1	6	17	US-10-806-924-859

ALIGNMENTS

RESULT 1

US-09-865-548A-39
; Sequence 39, Application US/09865548A
; Publication No. US20030096298A1
; GENERAL INFORMATION:
; APPLICANT: Barnea, Ilan
; APPLICANT: Beer, Ilan
; APPLICANT: Ziv, Tamar
; APPLICANT: Admon, Arie
; TITLE OF INVENTION: METHOD OF IDENTIFYING PEPTIDES CAPABLE OF BINDING TO MHC MOLECULES
; FILE REFERENCE: 01/22080
; CURRENT APPLICATION NUMBER: US/09/865,548A
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: US 60/290,958
; PRIOR FILING DATE: 2001-05-16
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-865-548A-39

Query Match 100.0%; Score 51; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLYDGMHEHL 9

Db 1 GLYDGMHEHL 9

```
RESULT 2
US-10-164-121A-13
; Sequence 13, Application US/10164121A
; Publication No. US20030228308A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Yi
; APPLICANT: Boon, Thierry
; APPLICANT: Van der Bruggen, Pierre
; APPLICANT: Traversari, Catra
; TITLE OF INVENTION: Isolated Peptides Which Bind to HLA-Cw6 Molecules And Uses Thereof
; FILE REFERENCE: LUD-5771
; CURRENT APPLICATION NUMBER: US/10/164,121A
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 36
; SEQ ID NO 13
; LENGTH: 9
; TYPE: PRT
; ORGANISM: H. sapiens
; FEATURE:
US-10-164-121A-13
Query Match 100.0%; Score 51; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GLYDGMHGL 9
Db 1 GLYDGMHGL 9

RESULT 3
US-10-164-078A-12
; Sequence 12, Application US/10164078A
; Publication No. US20030228325A1
; GENERAL INFORMATION:
; APPLICANT: Bilsborough, Janine
; APPLICANT: Schultz, Erwin
; APPLICANT: Panichelli, Christophe
; APPLICANT: Van der Bruggen, Pierre
; APPLICANT: Boon, Thierry
; TITLE OF INVENTION: Isolated Peptides Which Bind to HLA-B*8 Molecules And Uses Thereof
; FILE REFERENCE: LUD-5756
; CURRENT APPLICATION NUMBER: US/10/164,078A
; CURRENT FILING DATE: 2002-06-05
; NUMBER OF SEQ ID NOS: 35
; SEQ ID NO 12
; LENGTH: 9
; TYPE: PRT
; ORGANISM: H. sapiens
; FEATURE:
US-10-164-078A-12
Query Match 100.0%; Score 51; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GLYDGMHGL 9
Db 1 GLYDGMHGL 9

RESULT 4
US-10-447-161-29
; Sequence 29, Application US/10447161
; Publication No. US20040023314A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Rong-fu
; TITLE OF INVENTION: Mutant Fibronectin and Tumor Metastasis
; FILE REFERENCE: HO-P0248AUS1
; CURRENT APPLICATION NUMBER: US/10/447,161
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/383,530
```

```
; PRIOR FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-447-161-29
Query Match 100.0%; Score 51; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GLYDGMHGL 9
Db 1 GLYDGMHGL 9

RESULT 5
US-10-651-616-24
; Sequence 24, Application US/10651616
; Publication No. US20040253235A1
; GENERAL INFORMATION:
; APPLICANT: CytoCure, LLC
; APPLICANT: DURDA, PAUL
; APPLICANT: KURNICK, JAMES T.
; TITLE OF INVENTION: METHODS FOR UP-REGULATING ANTIGEN EXPRESSION IN TUMORS
; FILE REFERENCE: 027823-0305578
; CURRENT APPLICATION NUMBER: US/10/651,616
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: 60/407,492
; PRIOR FILING DATE: 2002-08-29
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Homo sapien artificial
US-10-651-616-24
Query Match 100.0%; Score 51; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GLYDGMHGL 9
Db 1 GLYDGMHGL 9

RESULT 6
US-10-362-715-8
; Sequence 8, Application US/10362715
; Publication No. US20040253574A1
; GENERAL INFORMATION:
; APPLICANT: Schuler, Gerold
; APPLICANT: Schuler-Thurner, Beatrice
; TITLE OF INVENTION: METHOD FOR READY-TO-USE, ANTIGEN LOADED OR UNLOADED,
; FILE REFERENCE: 1430/12
; CURRENT APPLICATION NUMBER: US/10/362,715
; CURRENT FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-362-715-8
```


Query Match 100.0%; Score 51; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLYDGMHHL 9
Db 1 GLYDGMHHL 9

RESULT 7
US-10-705-459-39
; Sequence 39, Application US/10705459
; Publication No. US20050053918A1
; GENERAL INFORMATION:
; APPLICANT: Barnea, Eilon
; APPLICANT: Beer, Ilan
; APPLICANT: Ziv, Tamar
; APPLICANT: Admon, Arie
; APPLICANT: Dassau, Lior
; APPLICANT: Buchsbaum, Samuel
; TITLE OF INVENTION: METHOD OF IDENTIFYING PEPTIDES CAPABLE OF BINDING TO MHC MOLECULES
; TITLE OF INVENTION: PEPTIDES IDENTIFIED THEREBY AND THEIR USES
; FILE REFERENCE: 26884
; CURRENT APPLICATION NUMBER: US/10/705,459
; CURRENT FILING DATE: 2003-11-12
; NUMBER OF SEQ ID NOS: 372
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide

US-10-705-459-39

Query Match 100.0%; Score 51; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLYDGMHHL 9
Db 1 GLYDGMHHL 9

RESULT 8
US-10-776-521B-392
; Sequence 392, Application US/10776521B
; Publication No. US20050202033A1
; GENERAL INFORMATION:
; APPLICANT: Fletchner, Jessica
; APPLICANT: Prince-Cohane, Kenya
; APPLICANT: Mehta, Sunil
; APPLICANT: Slusarewicz, Paul
; APPLICANT: Andjelic, Sofija
; APPLICANT: Barber, Brian
; TITLE OF INVENTION: IMPROVED HEAT SHOCK PROTEIN-BASED VACCINES AND
; TITLE OF INVENTION: IMMUNOTHERAPIES
; FILE REFERENCE: 8449-405-999
; CURRENT APPLICATION NUMBER: US/10/776,521B
; CURRENT FILING DATE: 2004-02-12
; PRIOR APPLICATION NUMBER: 60/503,417
; PRIOR FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: 60/463,746
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: 60/462,469
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 60/447,142
; PRIOR FILING DATE: 2003-02-13
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 392
; LENGTH: 9

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heat shock protein binding domain

US-10-776-521B-392

Query Match 100.0%; Score 51; DB 18; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLYDGMHHL 9
Db 1 GLYDGMHHL 9

RESULT 9
US-10-941-150A-13
; Sequence 13, Application US/10941150A
; Publication No. US20050226881A1
; GENERAL INFORMATION:
; APPLICANT: VAN DER BRUGGEN, Pierre
; APPLICANT: BOON-FALLEUR, Thierry
; APPLICANT: BRECKPOT, Karine
; APPLICANT: THIELEMANS, Kris
; TITLE OF INVENTION: ISOLATED PEPTIDE WHICH BINDS TO HLA-CW*07 AND USES THEREOF
; FILE REFERENCE: IJD-5853-US (10411307)
; CURRENT APPLICATION NUMBER: US/10/941,150A
; CURRENT FILING DATE: 2004-09-15
; PRIOR APPLICATION NUMBER: US 60/504,874
; PRIOR FILING DATE: 2003-09-22
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Derived from MAGEA10

US-10-941-150A-13

Query Match 100.0%; Score 51; DB 18; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLYDGMHHL 9
Db 1 GLYDGMHHL 9

RESULT 10
US-10-149-138-338
; Sequence 338, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Eteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0140001
; CURRENT APPLICATION NUMBER: US/10/149,138
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,299
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 338

```
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-338

Query Match          54.9%; Score 28; DB 15; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GMEHL 9
   |||||
Db 1 GMEHL 5

RESULT 11
US-10-149-138-901
; Sequence 901, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0140001
; CURRENT APPLICATION NUMBER: US/10/149,138
; PRIOR FILING DATE: 2002-06-10
; PRIOR FILING DATE: 2000-12-11
; PRIOR FILING DATE: 2000-12-11
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 901
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-901

Query Match          54.9%; Score 28; DB 15; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GMEHL 9
   |||||
Db 3 GMEHL 7

RESULT 12
US-10-149-138-2092
; Sequence 2092, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0140001
; CURRENT APPLICATION NUMBER: US/10/149,138
; CURRENT FILING DATE: 2002-06-10
```

```
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,299
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2092
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-2092

Query Match          54.9%; Score 28; DB 15; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GMEHL 9
   |||||
Db 1 GMEHL 5

RESULT 13
US-10-149-138-2681
; Sequence 2681, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0140001
; CURRENT APPLICATION NUMBER: US/10/149,138
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,299
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2681
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-2681

Query Match          54.9%; Score 28; DB 15; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GMEHL 9
   |||||
Db 3 GMEHL 7

RESULT 14
US-10-149-138-3329
; Sequence 3329, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
```

APPLICANT: Celis, Esteban
APPLICANT: Keogh, Elissa
TITLE OF INVENTION: Inducing Cellular Immune Responses to
TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 2060.0140001
CURRENT APPLICATION NUMBER: US/10/149,138
CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: PCT/US00/33591
PRIOR FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: US 09/458,299
PRIOR FILING DATE: 1999-12-11
NUMBER OF SEQ ID NOS: 4641
SOFTWARE: Patent in version 3.1
SEQ ID NO 3329
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-3329

Query Match 54.9%; Score 28; DB 15; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GMEHL 9
|
|
|
|
|
Db 3 GMEHL 7

RESULT 15
US-10-149-138-338
Sequence 338, Application US/10149138
Publication No. US20040121946A9
GENERAL INFORMATION:
APPLICANT: Fikes, John
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Celis, Esteban
APPLICANT: Keogh, Elissa
TITLE OF INVENTION: Inducing Cellular Immune Responses to
TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 2060.0140001
CURRENT APPLICATION NUMBER: US/10/149,138
CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: PCT/US00/33591
PRIOR FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: US 09/458,299
PRIOR FILING DATE: 1999-12-11
NUMBER OF SEQ ID NOS: 4641
SOFTWARE: Patent in version 3.1
SEQ ID NO 338
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-338

Query Match 54.9%; Score 28; DB 16; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GMEHL 9
|
|
|
|
|
Db 1 GMEHL 5

Search completed: November 15, 2005, 15:59:48
Job time : 163 secs

THIS PAGE BLANK (USPTO)

APPLICATION NUMBER: US 07/648205
FILING DATE: 01-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRF 114CIP
TELEPHONE: (404) 815-6508
TELEFAX: (404) 815-6555
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-335-198-22

Query Match 45.1%; Score 23; DB 1; Length 8;
Best Local Similarity 57.1%; Pred. NO. 4.1e+05;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LYDGMH 8
| | | |
Db 2 LLDGLEN 8

RESULT 15
US-09-420-211-12
; Sequence 12, Application US/09420211B
; Patent No. 6303330
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney B
; APPLICANT: Burke, Charles C
; APPLICANT: Wildung, Mark R
; TITLE OF INVENTION: GERANYL DIPHOSPHATE SYNTHASE LARGE SUBUNIT, AND METHODS
; TITLE OF INVENTION: OF USE
; FILE REFERENCE: WSUR14294
; CURRENT APPLICATION NUMBER: US/09/420,211B
; CURRENT FILING DATE: 1999-10-18
; EARLIER APPLICATION NUMBER: PCT/US98/21772
; EARLIER FILING DATE: 1998-10-15
; EARLIER APPLICATION NUMBER: 08/951,924
; EARLIER FILING DATE: 1997-10-16
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Mentha piperita
US-09-420-211-12

Query Match 45.1%; Score 23; DB 3; Length 8;
Best Local Similarity 80.0%; Pred. NO. 4.1e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLYDG 5
| | | |
Db 2 GLYQG 6

Search completed: November 15, 2005, 15:57:00
Job time : 42 secs

ADDRESS: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403.459
FILING DATE: Concurrently Herewith
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: UTSC:390/KIT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-403-459-19

Query Match 47.1%; Score 24; DB 4; Length 9;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GLYDGM 7
||| :
Db 1 GLYDGCQ 7

RESULT 12

US-09-462-453-14
Sequence 14, Application US/09462453
Patent No. 6723695
GENERAL INFORMATION:
APPLICANT: BURROWS, SCOTT RENTON
APPLICANT: KHANNA, RAJIV
APPLICANT: SHERRITT, MARTINA ALISON
TITLE OF INVENTION: CTL EPITOPES FROM EBV
FILE REFERENCE: FBRC:010
CURRENT APPLICATION NUMBER: US/09/462.453
CURRENT FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 14
LENGTH: 9
TYPE: PRT
ORGANISM: Epstein Barr Virus
US-09-462-453-14

Query Match 47.1%; Score 24; DB 4; Length 9;
Best Local Similarity 44.4%; Pred. No. 4.1e+05;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GLYDGMHL 9
||| :
Db 1 GLYERAHV 9

RESULT 13

PCT-US95-00147-72
Sequence 72, Application PC/TUS9500147

GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Substrate Specificity of Protein Kinases
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, suite 510
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00147
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/178,570
FILING DATE: JANUARY 7, 1994
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A., Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: BBI-004CPPC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
PCT-US95-00147-72

Query Match 47.1%; Score 24; DB 5; Length 9;
Best Local Similarity 42.9%; Pred. No. 4.1e+05;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLYDGM 7
||| :
Db 3 GIYEAL 9

RESULT 14

US-08-335-198-22
Sequence 22, Application US/08335198
Patent No. 5637454
GENERAL INFORMATION:
APPLICANT: Harley, John B.
TITLE OF INVENTION: Assays and Treatments for Autoimmune
Diseases
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kilpatrick & Cody
STREET: 1100 Peachtree Street, Ste. 2800
CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.
ZIP: 30309-4539
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/335,198
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
PCT-US95-00147-45

Query Match 47.1%; Score 24; DB 5; Length 8;
Best Local Similarity 42.9%; Pred. No. 4.1e+05;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLYDGM 7
|:|:|:
DB 2 GIYEAL 8

RESULT 8

US-08-178-570-72
; Sequence 72, Application US/08178570
; Patent No. 5532167

; GENERAL INFORMATION:

; APPLICANT: Lewis C. Cantley

; APPLICANT: Zhou Song Yang

; TITLE OF INVENTION: Substrate Specificity of Protein Kinases

; NUMBER OF SEQUENCES: 77

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD

; STREET: 60 STATE STREET, suite 510

; CITY: BOSTON

; STATE: MASSACHUSETTS

; COUNTRY: USA

; ZIP: 02109-1875

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: ASCII text

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/178,570

; FILING DATE: JANUARY 7, 1994

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: DeConti, Giulio A., Jr.

; REGISTRATION NUMBER: 31,503

; REFERENCE/DOCKET NUMBER: BBI-004

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 227-7400

; TELEFAX: (617) 227-5941

; INFORMATION FOR SEQ ID NO: 72:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 9 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; FRAGMENT TYPE: internal

US-08-178-570-72

Query Match 47.1%; Score 24; DB 1; Length 9;
Best Local Similarity 42.9%; Pred. No. 4.1e+05;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLYDGM 7
|:|:|:
DB 3 GIYEAL 9

RESULT 9

US-08-369-643-72

; Sequence 72, Application US/08369643A

; Patent No. 6004757

; GENERAL INFORMATION:

; APPLICANT: Cantley, Lewis C.
; APPLICANT: Songyang, Zhou
; TITLE OF INVENTION: Substrate Specificity of Protein Kinases
; FILE REFERENCE: CNS-001CP
; CURRENT APPLICATION NUMBER: US/08/369,643A
; CURRENT FILING DATE: 1995-01-06
; EARLIER APPLICATION NUMBER: US 08/178,570
; EARLIER FILING DATE: 1994-01-07
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 72
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Human enolase
; OTHER INFORMATION: (Y43)
US-08-369-643-72

Query Match 47.1%; Score 24; DB 3; Length 9;
Best Local Similarity 42.9%; Pred. No. 4.1e+05;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLYDGM 7
|:|:|:
DB 3 GIYEAL 9

RESULT 10

US-09-503-172A-3

; Sequence 3, Application US/09503172A

; Patent No. 6284510

; GENERAL INFORMATION:

; APPLICANT: ITO, Tetsuya

; APPLICANT: FUJITA, Koki

; APPLICANT: HARA, Kozo

; APPLICANT: TONOUZUKA, Takashi

; APPLICANT: SAKANO, Yoshiyuki

; TITLE OF INVENTION: BETA-FRUCTOFURANOSIDASE GENE

; FILE REFERENCE: 10749-0001-0

; CURRENT APPLICATION NUMBER: US/09/503,172A

; CURRENT FILING DATE: 2000-02-14

; PRIOR APPLICATION NUMBER: JP 160416/1999

; PRIOR FILING DATE: 1999-06-08

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 3

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Arthrobacter sp.

US-09-503-172A-3

Query Match 47.1%; Score 24; DB 3; Length 9;
Best Local Similarity 71.4%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GLYDGM 7
|:|:|:
DB 3 GLQDGP 9

RESULT 11

US-08-403-459-19

; Sequence 19, Application US/08403459

; Patent No. 6514942

; GENERAL INFORMATION:

; APPLICANT: Ioannides, Constantin G.

; APPLICANT: Fisk, Bryan A.

; APPLICANT: Ioannides, Maria G.

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STIMULATING

; TITLE OF INVENTION: T-LYMPHOCYTES

; NUMBER OF SEQUENCES: 68

; CORRESPONDENCE ADDRESS:

SEQUENCE CHARACTERISTICS:
 LENGTH: 8 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FRAGMENT TYPE: N-terminal
 FEATURE:
 LOCATION: 1
 OTHER INFORMATION: Xaa is glutamine or pyrrolidone
 OTHER INFORMATION: carboxylic acid.
 US-08-446-206B-25

Query Match 47.1%; Score 24; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 4.1e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 3 YDGM 6
 ||||
 Db 2 YDGM 5

RESULT 5
 US-08-807-030-11
 ; Sequence 11, Application US/08807030
 ; Patent No. 5817755
 ; GENERAL INFORMATION:
 ; APPLICANT: Eyre, David R.
 ; APPLICANT: Clemens, J. Daniel
 ; APPLICANT: Ochs, Vincent W.
 ; TITLE OF INVENTION: Synthetic Peptide Analogs of NTX
 ; NUMBER OF SEQUENCES: 74
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Christensen O'Connor Johnson & Kindness
 ; ADDRESSEE: PLLC
 ; STREET: 1420 Fifth Avenue, Suite 2800
 ; CITY: Seattle
 ; STATE: Washington
 ; COUNTRY: U.S.A.
 ; ZIP: 98101
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/807,030
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/446,206
 ; FILING DATE: 19-MAY-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Shelton, Dennis K.
 ; REGISTRATION NUMBER: 26,997
 ; REFERENCE/DOCKET NUMBER: WRO8110387
 ; TELEPHONE: 206 224 0718
 ; TELEFAX: 206 224 0779
 ; INFORMATION FOR SEQ ID NO: 11:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 8 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; FRAGMENT TYPE: N-terminal
 ; FEATURE:
 ; NAME/KEY: misc-feature
 ; LOCATION: 1
 ; OTHER INFORMATION: Xaa is pyroglutamic acid
 US-08-807-030-11

Query Match 47.1%; Score 24; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 4.1e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 3 YDGM 6
 ||||
 Db 2 YDGM 5

RESULT 6
 US-08-369-643-45
 ; Sequence 45, Application US/08369643A
 ; Patent No. 6004757
 ; GENERAL INFORMATION:
 ; APPLICANT: Cantley, Lewis C.
 ; APPLICANT: Songyang, Zhou
 ; TITLE OF INVENTION: Substrate Specificity of Protein Kinases
 ; FILE REFERENCE: CNS-001CP
 ; CURRENT APPLICATION NUMBER: US/08/369,643A
 ; CURRENT FILING DATE: 1995-01-06
 ; EARLIER APPLICATION NUMBER: US 08/178,570
 ; EARLIER FILING DATE: 1994-01-07
 ; NUMBER OF SEQ ID NOS: 92
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 45
 ; LENGTH: 8
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:Enolase (Y43)
 US-08-369-643-45

Query Match 47.1%; Score 24; DB 3; Length 8;
 Best Local Similarity 42.9%; Pred. No. 4.1e+05;
 Matches 3; Conservative 1; Indels 0; Gaps 0;

QY 1 GLYDGM 7
 ||:|
 Db 2 GIYEAL 8

RESULT 7
 PCT-US95-00147-45
 ; Sequence 45, Application PC/TUS9500147
 ; GENERAL INFORMATION:
 ; APPLICANT:
 ; TITLE OF INVENTION: Substrate Specificity of Protein Kinases
 ; NUMBER OF SEQUENCES: 88
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LAHIVE & COCKFIELD
 ; STREET: 60 STATE STREET, suite 510
 ; CITY: BOSTON
 ; STATE: MASSACHUSETTS
 ; COUNTRY: USA
 ; ZIP: 02109-1875
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: ASCII text
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/00147
 ; FILING DATE:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/178,570
 ; FILING DATE: JANUARY 7, 1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: DeConti, Giulio A., Jr.
 ; REGISTRATION NUMBER: 31,503
 ; REFERENCE/DOCKET NUMBER: BBI-004CPPC
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 227-7400
 ; TELEFAX: (617) 227-5941


```

; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/178,570
; FILING DATE: JANUARY 7, 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A., Jr.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: BBI-004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; US-08-178-570-45
;
; Query Match 47.1%; Score 24; DB 1; Length 8;
; Best Local Similarity 42.9%; Pred No. 4,1e+05;
; Matches 3; Conservative 3; Mismatches 1; Indels
;
; QY 1 GLYDGM 7
; |::|
; DB 2 GYEALE 8
;
; RESULT 4
; US-08-446-206B-25
; Sequence 25, Application US/08446206B
; Patent No. 5750647
; GENERAL INFORMATION:
; APPLICANT: Eyre, David R
; APPLICANT: Clemens, J Daniel
; APPLICANT: Ochs, Vincent W
; TITLE OF INVENTION: Synthetic Peptide Analogs of NTX
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Christensen, O'Connor, Johnson & Kindness PLLC
; STREET: 1420 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: WA 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,206B
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Shelton, Dennis K
; REGISTRATION NUMBER: 26,997
; REFERENCE/DOCKET NUMBER: WROS18360
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206 682 8100
; TELEFAX: 206 224 0779
; TELEX:
; INFORMATION FOR SEQ ID NO: 25:

```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 15, 2005, 15:45:59 ; Search time 41 Seconds
(without alignments)
16.386 Million cell updates/sec

Title: US-09-856-812B-42

Perfect score: 51

Sequence: 1 GLYDGMHL 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 99282

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	49.0	8	1	US-08-571-985-22
2	25	49.0	8	2	US-09-116-766-22
3	24	47.1	8	1	US-08-178-570-45
4	24	47.1	8	1	US-08-446-206B-25
5	24	47.1	8	2	US-08-807-030-11
6	24	47.1	8	3	US-08-369-643-45
7	24	47.1	8	5	PCT-US95-00147-45
8	24	47.1	9	1	US-08-178-570-72
9	24	47.1	9	3	US-08-369-643-72
10	24	47.1	9	3	US-08-503-172A-3
11	24	47.1	9	4	US-08-403-459-19
12	24	47.1	9	4	US-09-462-453-14
13	24	47.1	9	5	PCT-US95-00147-72
14	23	45.1	8	3	US-08-335-198-22
15	23	45.1	8	3	US-09-420-211-12
16	23	45.1	9	2	US-08-951-924A-3
17	22	43.1	6	2	US-07-718-577-20
18	22	43.1	6	3	US-09-198-092-4
19	22	43.1	8	3	US-08-477-928A-47
20	22	43.1	8	3	US-09-128-572-13
21	22	43.1	8	4	US-09-782-385A-13
22	22	43.1	9	1	US-08-186-266-11
23	22	43.1	9	4	US-09-593-870A-30
24	22	43.1	9	5	PCT-US95-04975-6
25	21	41.2	7	1	US-08-285-936-49
26	21	41.2	7	1	US-08-487-860-49
27	21	41.2	7	2	US-08-310-912A-127
					Sequence 22, Appl
					Sequence 22, Appl
					Sequence 45, Appl
					Sequence 25, Appl
					Sequence 11, Appl
					Sequence 45, Appl
					Sequence 72, Appl
					Sequence 72, Appl
					Sequence 3, Appl
					Sequence 19, Appl
					Sequence 14, Appl
					Sequence 72, Appl
					Sequence 12, Appl
					Sequence 3, Appl
					Sequence 20, Appl
					Sequence 4, Appl
					Sequence 47, Appl
					Sequence 13, Appl
					Sequence 13, Appl
					Sequence 11, Appl
					Sequence 30, Appl
					Sequence 6, Appl
					Sequence 49, Appl
					Sequence 47, Appl
					Sequence 127, App

Sequence 127, App
Sequence 127, App
Sequence 45, Appl
Sequence 12, Appl
Sequence 1, Appl
Sequence 2, Appl
Sequence 3, Appl
Sequence 4, Appl
Sequence 10, Appl
Sequence 12, Appl
Sequence 22, Appl
Sequence 31, Appl
Sequence 3, Appl
Sequence 5, Appl
Sequence 31, Appl
Sequence 7, Appl
Sequence 41, Appl

ALIGNMENTS

RESULT 1

US-08-571-985-22
; Sequence 22, Application US/08571985
; Patent No. 5783557
; GENERAL INFORMATION:
; APPLICANT: Burstein, Yigal
; APPLICANT: Trainin, Nathan
; APPLICANT: Rycus, Avigail
; TITLE OF INVENTION: THP-gamma2 Analogs and Pharmaceutical
; TITLE OF INVENTION: Compositions Comprising Them
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kohn & Associates
; STREET: 30500 No. 5783557thwestern Hwy., Suite 410
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: USA
; ZIP: 48334
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/571,985
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 106214
; FILING DATE: 01-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I
; REGISTRATION NUMBER: 30,955
; REFERENCE/DOCKET NUMBER: 2163.00048
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810) 539-5050
; TELEFAX: (810) 539-5055
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-571-985-22

Query Match 49.0%; Score 25; DB 1; Length 8;
Best Local Similarity 62.5%; Pred. No. 4.1e+05;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LYDGMHL 9

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 15, 2005, 15:40:18 ; Search time 162 Seconds
(without alignments)
21.487 Million cell updates/sec

Title: US-09-856-812B-42

Perfect score: 51

Sequence: 1 GLYDGMHL 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 330156

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	51	100.0	9	3 AAY71487	Aay71487 Human MAG
2	51	100.0	9	4 AAB31323	Aab31323 Exemplary
3	51	100.0	9	5 AAO17088	Aao17088 Human mag
4	51	100.0	9	6 ABJ19876	Abj19876 MHC bindi
5	51	100.0	9	8 ADG89586	Adg89586 Class I H
6	51	100.0	9	8 ADI19869	Adi19869 Human HLA
7	51	100.0	9	8 ADI19026	Adi19026 Human HLA
8	51	100.0	9	8 ADJ58374	Adj58374 Peptide p
9	51	100.0	9	8 ADL26560	Adl26560 Melanoma
10	51	100.0	9	8 ADR59760	Adr59760 Novel hyb
11	41	80.4	9	3 AAY71488	Aay71488 Human MAG
12	34	66.7	6	5 ABG79151	Abg79151 Human MAG
13	32	62.7	9	2 AAY46134	Aay46134 Immunogen
14	31	60.8	9	2 AAY46090	Aay46090 Immunogen
15	28	54.9	9	2 AAY46489	Aay46489 Immunogen
16	28	54.9	9	2 AAY46037	Aay46037 Immunogen
17	28	54.9	9	2 AAY46435	Aay46435 Immunogen
18	28	54.9	9	4 AAG88669	Aag88669 HER2/NEU
19	28	54.9	9	4 AAG88319	Aag88319 HER2/NEU
20	28	54.9	9	6 ABJ19990	Abj19990 MHC bindi
21	28	54.9	9	8 ADP25980	Adp25980 Plasmodiu
22	27	52.9	9	7 ADE78951	Ade78951 Interleuk
23	27	52.9	9	7 ADE78688	Ade78688 Interleuk
24	27	52.9	9	7 ADE78950	Ade78950 Interleuk
25	27	52.9	9	8 ADH48474	Adh48474 HLA-A*02

ALIGNMENTS

RESULT 1

AAY71487

ID AAY71487 standard; peptide; 9 AA.

XX AC AAY71487;

DT 12-OCT-2000 (first entry)

XX DE Human MAGE-A10 nonapeptide-1.

XX KW MAGE-A10; human; Tumour Rejection Antigen; TRA; Human Leucocyte Antigen;

XX KW HLA; Major Histocompatibility Complex; MHC; cytolytic T-lymphocyte; CTL;

XX KW immune response stimulator; prophylaxis; therapy; diagnosis; tumour;

XX KW cancer; TNF; tumour necrosis factor; vaccine; cytostatic.

XX OS Homo sapiens.

XX PN WO200032769-A2.

XX PD 08-JUN-2000.

XX PF 26-NOV-1999; 99WO-IB002018.

XX PR 27-NOV-1998; 98GB-00026143.

XX PA (LUDW-) LUDWIG INST CANCER RES.

XX PI Huang L, Van Pel A, Brasseur F, De Plaen E, Boon T;

XX DR WPI; 2000-412317/35.

XX PT Novel polypeptides expressed in tumor cells useful for treating cancers
PT have an ability to complex with a major histocompatibility complex
PT molecule and comprises a specific unbroken amino acid sequence.

XX PS Claim 8; Page 36; 80pp; English.

XX CC The patent discloses MAGE-A10 and MAGE-A8 polypeptide, nonapeptide and
XX CC decapeptide sequences, that function as tumour rejection antigens (TRA).
XX CC These peptides are capable of forming a complex with major
XX CC histocompatibility complex (MHC) molecule type HLA-A2.1 (Human Leucocyte
XX CC Antigen), that are recognised by T-lymphocytes and elicit an immune
XX CC response from cytolytic T-lymphocytes (CTL). They function as an immune
XX CC response stimulator. Tumour rejection antigens are useful in prophylaxis,
XX CC therapy and diagnosis of tumours and are effective in controlling or
XX CC preventing tumour growth. The present peptide sequence is the human MAGE-
XX CC A10 nonapeptide-1, that corresponds to residues 254-262 of the MAGE-A10
XX CC protein. This peptide can serve as a tumour rejection antigen (TRA) and

Abg79016 Human MAG
Adb79001 Human ant
Aau26647 Human Leu
Aau26980 Human Leu
Abg77556 Targettin
Aar59204 Peptide f
Aar73323 Human TSH
Aar73322 Human TSH
Adc81364 Bovin THF
Adk65307 Human NRP
Adk65261 Human NRP
Ado37836 Binding p
Ado28358 Capture s
Aar50535 6-mer pep
Aar79690 pp60(c-ar
Aaw08241 Analogue
Aay57991 Enolase
Aar79715 pp92(c-fp
Aay10570 HLA Class
Aay47762 Immunogen

26 51.0 6 5 ABG79016
27 51.0 8 7 ADB79001
28 51.0 9 4 AAU26647
29 51.0 9 4 AAU26980
30 49.0 7 5 ABG77556
31 49.0 8 2 AAR59204
32 49.0 8 2 AAR73323
33 49.0 8 2 AAR73322
34 49.0 8 2 ADC81364
35 49.0 8 2 ADK65307
36 49.0 9 7 ADK65261
37 47.1 6 8 ADO37836
38 47.1 6 8 ADO28358
39 47.1 6 8 AAR50535
40 47.1 8 2 AAR79690
41 47.1 8 2 AAW08241
42 47.1 8 3 AAY57991
43 47.1 9 2 AAR79715
44 47.1 9 2 AAY10570
45 47.1 9 2 AAY47762

CC in combination with adjuvants, can produce vaccines useful for treating a
 CC variety of tumours that express MAGE-A10
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 51; DB 3; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GLYDGMHL 9
 |||||
 Db 1 GLYDGMHL 9

RESULT 2
 AAB31323
 ID AAB31323 standard; peptide; 9 AA.
 XX
 AC AAB31323;
 XX
 DT 20-APR-2001 (first entry)
 XX
 DE Exemplary antigen characteristic of tumours and derived from MAGE-A10.
 XX
 KW MAGE-A1; HLA; human leukocyte antigen; CD4+ T lymphocyte; cancer;
 KW MAGE-A1 HLA class II-binding protein; vaccine.
 XX
 OS Homo sapiens.
 XX
 PN WO200078806-A1.
 XX
 PD 28-DEC-2000.
 XX
 PF 14-JUN-2000; 2000WO-US016287.
 XX
 PR 18-JUN-1999; 99US-00336091.
 XX
 PA (LUDW-) LUDWIG INST CANCER RES.
 XX
 PI Van Snick J, Lethe B, Chaux P, Boon-Palleur T, Van Der Bruggen P;
 XX
 DR WPI; 2001-102698/11.
 XX

Novel MAGE-A1 human leukocyte antigen class II peptides which bind to and
 are presented to the class II molecules, useful for inducing immune
 response and treating cancers characterized by expression of MAGE-A1.

XX Disclosure; Page 32; 78pp; English.

XX AAB31302-59 represent exemplary antigens which are characteristic of
 CC tumours. They can be used to enhance the immune response of vaccines
 CC comprising peptides derived from human MAGE-A1 HLA (human leukocyte
 CC antigen) class II-binding protein. Peptides derived from the MAGE-A1 HLA
 CC binding protein stimulate the activity and proliferation of CD4+ T
 CC lymphocytes. The MAGE-A1 HLA binding protein is useful as a diagnostic
 CC agent for diagnosing a disorder characterized by expression of MAGE-A1.
 CC The protein is used for treating a disorder characterized by expression
 CC of MAGE-A1 such as cancers e.g. melanoma, squamous cell carcinomas,
 CC colorectal carcinomas, osteosarcomas, and lymphocytic leukemias. Peptides
 CC derived from the MAGE-A1 HLA binding protein are useful in the production
 CC of anti-tumour vaccines
 XX

SQ Sequence 9 AA;

Query Match 100.0%; Score 51; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLYDGMHL 9
 |||||
 Db 1 GLYDGMHL 9

RESULT 3
 AAO17088
 ID AAO17088 standard; peptide; 9 AA.
 XX
 AC AAO17088;
 XX
 DT 06-JUN-2002 (first entry)
 XX
 DE Human mage-A10 protein antigen SEQ ID NO: 8.

XX Cryopreserved mature dendritic cell; antigen; vaccine; cytostatic;
 KW virucide; cancer; hepatitis B virus.
 XX
 OS Homo sapiens.

XX WO200216560-A1.
 PN
 XX
 PD 28-FEB-2002.
 XX

XX 24-AUG-2001; 2001WO-EP009790.
 PF

XX 24-AUG-2000; 2000DE-01041515.
 PR

XX (SCHU/) SCHULER G.
 PA

XX Schuler G, Schuler-Thurner B;
 PI

XX WPI; 2002-292062/33.
 DR

XX Preparation of cryopreserved, mature dendritic cells, useful in vaccines,
 PT comprises culturing immature cells on medium containing cocktail of
 PT maturation factors, then freezing.
 XX

XX Disclosure; Fig 28; 87pp; German.

XX The present invention relates to a method for the preparation of ready-
 CC for-use, cryopreserved, mature dendritic cells comprising growing
 CC immature dendritic cells in a culture medium that includes a 'maturation
 CC cocktail' of one or more maturation stimuli and freezing the resulting
 CC matured cells in a freezing medium that does not contain heterologous
 CC serum. When loaded with antigens, the dendritic cells can be used as
 CC vaccines, e.g. against tumours and hepatitis B virus. The present
 CC sequence is an antigen described in the invention
 XX

SQ Sequence 9 AA;

Query Match 100.0%; Score 51; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLYDGMHL 9
 |||||
 Db 1 GLYDGMHL 9

RESULT 4

ABJ19876
 ID ABJ19876 standard; peptide; 9 AA.
 XX

XX ABJ19876;
 AC

XX 10-APR-2003 (first entry)
 DT

XX MHC binding peptide SEQ ID No 39.
 DE

XX Antirheumatic; antiallergic; antiarthritic; nootropic; neuroprotective;
 KW antiinflammatory; major histocompatibility complex; MHC;
 KW autoimmune disease; T cell; B cell; allergic disease; multiple sclerosis;
 KW rheumatoid arthritis; neurodegenerative disorder; Alzheimer's disease;
 KW inflammation; gene therapy; MHC binding peptide.
 XX

OS Synthetic.
 XX

PN WO200294981-A2.
XX 28-NOV-2002.
XX 16-MAY-2002; 2002WO-IL000383.
XX 16-MAY-2001; 2001US-0290958P.
PR 29-MAY-2001; 2001US-00865548.
XX (TECR) TECHNION RES & DEV FOUND LTD.
XX Barnea E, Beer I, Ziv T, Admon A, Dasseau L, Buchsbaum S;
XX WPI; 2003-210043/20.
XX Identifying peptides that are capable of binding to major
PT histocompatibility complex (MHC) molecules of a particular haplotype by
PT analyzing peptides bound to the soluble and secreted form of the MHC
PT molecules of the particular haplotype.
XX Example; Fig 5D; 238pp; English.
XX The invention relates to a novel method for identifying peptides
CC originating from a particular cell type, which are capable of binding to
CC major histocompatibility complex (MHC) molecules of a particular
CC haplotype. The method comprises analysing peptides bound to the soluble
CC and secreted form of the MHC molecules of the particular haplotype. The
CC method is useful for identifying peptides for treating an autoimmune
CC disease, such as T or B cell and/or allergic disease or condition,
CC rheumatoid arthritis, or multiple sclerosis, neurodegenerative disorders,
CC e.g. Alzheimer's disease, or diseases associated with inflammation. The
CC sequences of the invention may be used in a gene therapy application.
CC This sequence represents a peptide relating to the method for identifying
CC MHC binding peptides of the invention
XX
XX SQ Sequence 9 AA;
Query Match 100.0%; Score 51; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GLYDGMHEHL 9
Db 1 GLYDGMHEHL 9
RESULT 5
ADG89586
ID ADG89586 standard; peptide; 9 AA.
AC ADG89586;
XX 11-MAR-2004 (first entry)
DT Class I HLA-restricted testis cancer antigen #21.
DE metastatic cancer cell differentiation; mutated fibronectin;
XX metastatic cancer; class I HLA-restricted; testis; cancer antigen.
KW Unidentified.
XX OS
XX WO2003100027-A2.
XX 04-DEC-2003.
XX 28-MAY-2003; 2003WO-US016736.
XX 28-MAY-2002; 2002US-0363530P.
XX (BAYU) BAYLOR COLLEGE MEDICINE.
XX Wang R;
XX

DR WPI; 2004-035134/03.
XX Identifying a cell that differentiates into a metastatic cancer cell,
PT useful for preventing metastatic cancer, comprises identifying a mutated
PT fibronectin in the cell.
XX Disclosure; SEQ ID NO 29; 137pp; English.
XX The invention comprises a method for identifying a cell that will
CC differentiate into a metastatic cancer cell, the method involves
CC identifying a mutated fibronectin in the cell. The method of the
CC invention is useful for preventing metastatic cancer. The present amino
CC acid sequence represents a Class I HLA-restricted testis cancer antigen.
XX
XX SQ Sequence 9 AA;
Query Match 100.0%; Score 51; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GLYDGMHEHL 9
Db 1 GLYDGMHEHL 9
RESULT 6
ADI19869
ID ADI19869 standard; peptide; 9 AA.
XX ADI19869;
XX 22-APR-2004 (first entry)
DT Human HLA-B18 binding MAGE-3 peptide #11.
XX Human HLA-B18 binding MAGE-3 peptide #11.
DE
XX HLA; human leucocyte antigen; melanoma; lung cancer; head cancer;
KW neck cancer; MAGE-3; human.
XX Homo sapiens.
OS US2003228325-A1.
XX 11-DEC-2003.
XX 05-JUN-2002; 2002US-00164078.
XX 05-JUN-2002; 2002US-00164078.
XX (BILS/) BILSBOROUGH J.
PA (SCHU/) SCHULTZ E.
PA (PANI/) PANICHELLI C.
PA (BOON/) BOON-FALLEUR T.
PA (BRUG/) BRUGEN P V D.
XX Bilsborough J, Schultz E, Panichelli C, Boon-Falleur T;
PI Bruggen PVD;
PI WPI; 2004-042211/04.
DR
XX Treating subject with pathological condition having human leucocyte
PT antigen-B18 molecules presented on cell surface by administering peptides
PT to subject for generating immunologically active response against cells.
XX Claim 22; SEQ ID NO 12; 15pp; English.
XX The present invention relates to a peptide which binds HLA (human
CC leucocyte antigen)-B18 to form T-cell epitope. The invention is useful
CC for treating a pathological conditions such as melanoma, lung cancer and
CC head and neck cancer. The present sequence is human HLA-B18 binding MAGE-
CC 3 peptide.
XX
XX SQ Sequence 9 AA;

```

Query Match      100.0%; Score 51; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLYDGMHL 9
Db 1 GLYDGMHL 9

RESULT 7
ADJ58374
ID ADJ58374 standard; peptide; 9 AA.
XX AC
XX ADJ58374;
XX DT 22-APR-2004 (first entry)
XX DE Human HLA-Cw6 binding MAGE-1 peptide #11.
XX KW MHC; major histocompatibility; therapy; cancer; melanoma; HLA-Cw6; human;
XX KW MAGE-1; cytostatic.
XX OS Homo sapiens.
XX PN US2003228308-A1.
XX PD 11-DEC-2003.
XX PF 05-JUN-2002; 2002US-00164121.
XX PR 05-JUN-2002; 2002US-00164121.
XX PA (ZHAN//) ZHANG Y.
XX PA (TRAV//) TRAVERSARI C.
XX PA (BOON//) BOON-FALLEUR T.
XX PA (BRUG//) BRUGGEN P V D.
XX PI Zhang Y, Traversari C, Boon-Falleur T, Bruggen PVD;
XX WPI; 2004-042210/04.
XX DT Treating subject with pathological condition having human leukocyte
XX PT antigen-Cw6 molecules presented on cell surface by administering peptides
XX PT to subject for generating immunologically active response against cells.
XX PS Example 7; SEQ ID NO 13; 15pp; English.
XX CC The present invention relates to peptides which form immunologically
XX CC active complexes with MHC molecules. The invention is useful for treating
XX CC a subject with pathological condition such as cancer which is melanoma by
XX CC presenting HLA-Cw6 molecules on the cell surface. The present sequence is
XX CC human HLA-Cw6 binding MAGE-1 peptide.
XX SQ Sequence 9 AA;

Query Match      100.0%; Score 51; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLYDGMHL 9
Db 1 GLYDGMHL 9

RESULT 8
ADJ58374
ID ADJ58374 standard; peptide; 9 AA.
XX AC
XX ADJ58374;
XX DT 06-MAY-2004 (first entry)
XX DE Peptide predicted to bind to HLA-A2 #34.
XX
```

```

XX KW major histocompatibility complex; MHC; cytolytic T-cell; HLA-A2;
XX KW Cytostatic; cancer.
XX OS Synthetic.
XX PN WO2004011483-A2.
XX PD 05-FEB-2004.
XX PF 23-JUL-2003; 2003WO-US023306.
XX PR 31-JUL-2002; 2002US-0400076P.
XX PA (LUDW-) LUDWIG INST CANCER RES.
XX PA (TORR-) TORREY PINES INST MOLECULAR STUDIES.
XX PI Valmori D, Ayyoub M, Pinilla C;
XX WPI; 2004-143815/14.
XX DT New isolated SSX-2 and SSX-2-related peptides that bind to human
XX PT leukocyte antigen (HLA) molecules, useful for diagnosing or treating
XX PT cancer, particularly melanoma.
XX PS Example 8; SEQ ID NO 34; 20pp; English.
XX CC The present invention relates to an isolated peptide which binds to a
XX CC major histocompatibility complex (MHC) molecule to form a complex that is
XX CC recognized by a cytolytic T-cell which recognizes and lyses cells
XX CC presenting complexes of HLA-A2 molecules comprising a sequence of 9 amino
XX CC acids fully defined in the specification, with the proviso that the
XX CC peptide is not the peptide of S17 itself. Specifically claimed is an HLA-
XX CC binding peptide comprising a sequence of 9 amino acids fully defined in
XX CC the specification. The composition and methods are useful for diagnosing
XX CC or treating cancer, particularly melanoma. The present sequence
XX CC represents a peptide predicted to bind to HLA-A2.
XX SQ Sequence 9 AA;

Query Match      100.0%; Score 51; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLYDGMHL 9
Db 1 GLYDGMHL 9

RESULT 9
ADL26560
ID ADL26560 standard; peptide; 9 AA.
XX AC
XX ADL26560;
XX DT 03-JUN-2004 (first entry)
XX DE Melanoma cell line MAGE gene encoded HLA-A2 peptide.
XX KW cytostatic; gene therapy; vaccine; cancer; immune response.
XX OS Homo sapiens.
XX PN WO2004019886-A2.
XX PD 11-MAR-2004.
XX PF 29-AUG-2003; 2003WO-US027125.
XX PR 29-AUG-2002; 2002US-0407492P.
XX PA (CYTO-) CYTOCURE LLC.
XX
```

PI Durda PJ, Kurnick JT, Dunn IS;
XX WPI; 2004-239114/22.
XX Increasing an immune response against a tumor cell comprises
PT administering to a subject with a tumor an amount of IFN-beta receptor
PT agonist and tumor associated antigen (TAA).
XX
XX Example 7; Page 47; 80pp; English.
XX The present invention relates to a method of increasing an immune
CC response against a tumour cell, comprising administering to a subject
CC with a tumour an amount of IFN-beta receptor agonist and tumour
CC associated antigen (TAA). The method is useful for increasing an immune
CC response against a tumour cell. The present sequence is a peptide used in
CC the exemplification of the invention.
XX
XX Sequence 9 AA;
SQ Query Match 100.0%; Score 51; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GLYDGMHL 9
Db 1 GLYDGMHL 9
|||||
1 GLYDGMHL 9
RESULT 10
ADR69760
ID ADR69760 standard; peptide; 9 AA.
XX ADR69760;
AC
XX 18-NOV-2004 (first entry)
DT
DE Novel hybrid antigen-related peptide #1340.
XX
XX hybrid antigen; antigenic domain; infectious agent; tumour antigen;
KW binding domain; heat shock protein; antimicrobial; cytostatic; vaccine;
KW gene therapy; infectious disease; cancer.
XX
XX Unidentified.
OS
XX WO2004071457-A2.
XX
XX 26-AUG-2004.
PD
XX 13-FEB-2004; 2004WO-US004340.
PF
XX 13-FEB-2003; 2003US-0447142P.
PR
XX 11-APR-2003; 2003US-0462469P.
PR
XX 18-APR-2003; 2003US-0463746P.
PR
XX 16-SEP-2003; 2003US-0503417P.
PR
XX 12-FEB-2004; 2004US-00776521.
XX
XX (MOJA-) MOJAVE THERAPEUTICS INC.
XX
XX Fletcher J, Prince-Cohane K, Mehta S, Slusarewicz P, Andjelic S;
PI Barber B;
XX
XX WPI; 2004-625768/60.
DR
XX New hybrid antigens comprising an antigenic domain and improved heat
PT shock protein-binding domains, useful for preventing or treating
PT infectious diseases or cancer.
XX
XX Example 11; Page 44; 56pp; English.
XX
XX This invention relates to a novel hybrid antigen which comprises at least
CC one antigenic domain of an infectious agent or tumour antigen and a
CC binding domain that non-covalently binds to a heat shock protein. The
CC invention may be useful for the production of compounds with an

CC antimicrobial or cytostatic activity. In addition, the invention may
CC prove useful for the production of a vaccine or for gene therapy. The
CC composition and methods disclosed are useful for preventing or treating
CC infectious diseases or cancer. The present sequence is that of a peptide
CC which was used in the exemplification of the invention.
XX
XX Sequence 9 AA;
SQ Query Match 100.0%; Score 51; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GLYDGMHL 9
Db 1 GLYDGMHL 9
|||||
1 GLYDGMHL 9
RESULT 11
AAV71488
ID AAV71488 standard; peptide; 9 AA.
XX AAV71488;
AC
XX 12-OCT-2000 (first entry)
DT
XX Human MAGE-A8 nonapeptide-1.
DE
XX MAGE-A8; human; Tumour Rejection Antigen; TRA; Human Leucocyte Antigen;
KW HLA; Major Histocompatibility Complex; MHC; cytolytic T-lymphocyte; CTL;
KW immune response stimulator; prophylaxis; therapy; diagnosis; tumour;
KW cancer; TNF; tumour necrosis factor; vaccine; cytostatic.
XX
XX Homo sapiens.
OS
XX WO200032769-A2.
PN
XX 08-JUN-2000.
PD
XX 26-NOV-1999; 99WO-IB002018.
PF
XX 27-NOV-1998; 98GB-00026143.
PR
XX (LUDW-) LUDWIG INST CANCER RES.
PA
XX Huang L, Van Pel A, Brasseur P, De Plaen E, Boon T;
PI WPI; 2000-412317/35.
XX
XX Novel polypeptides expressed in tumor cells useful for treating cancers
PT have an ability to complex with a major histocompatibility complex
PT molecule and comprises a specific unbroken amino acid sequence.
XX
XX Claim 8; Page 36; 80pp; English.
PS
XX The patent discloses MAGE-A10 and MAGE-A8 polypeptide, nonapeptide and
CC decapeptide sequences, that function as tumour rejection antigens (TRAS).
CC These peptides are capable of forming a complex with major
CC histocompatibility complex (MHC) molecule type HLA-A2.1 (Human Leucocyte
CC Antigen), that are recognised by T-lymphocytes and elicit an immune
CC response from cytolytic T-lymphocytes (CTL). They function as an immune
CC response stimulator. Tumour rejection antigens are useful in prophylaxis,
CC therapy and diagnosis of tumours and are effective in controlling or
CC preventing tumour growth. The present peptide sequence is the human MAGE-
CC A8 nonapeptide-1, that corresponds to residues 232-240 of the MAGE-A8
CC protein. This peptide can serve as a tumour rejection antigen (TRA) and
CC in combination with adjuvants, can produce vaccines useful for treating a
CC variety of tumours that express MAGE-A8
XX
XX Sequence 9 AA;
SQ Query Match 80.4%; Score 41; DB 3; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.8e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLYDGMH 8 66.7%; Score 34; DB 5; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 GLYDGREH 8
 1 GLYDGMH 6
 1 GLYDGM 6

RESULT 12
 ABG79151
 ID ABG79151 standard; peptide; 6 AA.
 AC ABG79151;
 XX
 XX 15-NOV-2002 (first entry)
 DT
 DE Human MAGE-A10 class I HLA restricted testis cancer antigen peptide #1.
 XX
 XX Cell penetrating peptide; cancer; tumour; melanoma; thymoma; antigen;
 KW lymphoma; sarcoma; lung cancer; non-Hodgkin's lymphoma; leukaemia;
 KW Hodgkin's lymphoma; uterine cancer; cervical cancer; bladder cancer;
 KW kidney cancer; adenocarcinoma; breast cancer; prostate cancer;
 KW ovarian cancer; pancreatic cancer; epitope; vaccine; dendritic cell;
 KW tumour infiltrating lymphocyte; TIL; human leukocyte antigen; HLA;
 KW cytostatic; human.
 XX
 OS Homo sapiens.
 OS Unidentified.
 OS
 XX
 PN WO200264057-A2.
 XX
 XX 22-AUG-2002.
 PD
 PF 15-FEB-2002; 2002WO-US005212.
 XX
 PR 15-FEB-2001; 2001US-0268687P.
 XX
 PA (BAYU) BAYLOR COLLEGE MEDICINE.
 XX
 PI Wang R;
 XX
 DR WPI; 2002-627577/67.
 XX
 PT Novel composition for treating a disease in an animal, comprises an
 PT immune effector cell and cell penetrating peptide associated with an
 PT antigen or antibody.
 XX
 PS Disclosure; Page 14; 61pp; English.
 XX

The invention relates to a composition (I) comprising an immune effector cell and a cell penetrating peptide (CPP) associated with an antigen or antibody. Also included are (i) a vaccine comprising (I), CPP associated with an antigen, and a pharmaceutically acceptable carrier and (2) preparing a composition for a disease, by providing (I) and CPP associated with an antigen for disease, and introducing the antigen-associated CPP to (I), where antigen enters into the cell. The antigens are, for example, tumour antigen derived epitopes recognised by tumour infiltrating lymphocytes (TIL) of HLA (human leukocyte antigen) class I or II. The composition is useful for enhancing immunity in an animal to a disease, by administering a mature dendritic cell comprising CPP associated with an antigen to disease, to the animal, such that following the administration, animal is protected from disease, where the animal comprises both CD4+ and CD8+ T cells. It is also useful for treating a disease (e.g. cancer, tumour, melanoma, thymoma, lymphoma, sarcoma, lung cancer, non-Hodgkin's lymphoma, leukaemia, Hodgkin's lymphoma, uterine cancer, cervical cancer, bladder cancer, kidney cancer, adenocarcinoma, breast cancer, prostate cancer, ovarian cancer and pancreatic cancer). The animal is further subjected to a cancer treatment including surgery, radiation, chemotherapy or gene therapy. The administration of (I), preferably dendritic cell is prior to, subsequent to or concurrent with, the cancer treatment. The present sequence is a tumour antigen derived epitope for inclusion in the composition of the invention

Sequence 6 AA;

Query Match 62.7%; Score 32; DB 2; Length 9;
 Best Local Similarity 71.4%; Pred. No. 1.8e+06;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLYDGMH 8 66.7%; Score 34; DB 5; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 GLYDGREH 8
 1 GLYDGMH 6
 1 GLYDGM 6

RESULT 13
 AAY46134
 ID AAY46134 standard; peptide; 9 AA.
 XX
 XX AAY46134;
 AC
 XX 01-DEC-1999 (first entry)
 DT
 DE Immunogenic peptide having a human leukocyte antigen binding motif #745.
 XX
 XX Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
 KW immune response; T cell activation; major histocompatibility complex;
 KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
 KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
 KW vaccine; immunisation.
 KW
 XX Synthetic.
 OS Homo sapiens.
 OS
 XX WO9945954-A1.
 PN
 XX 16-SEP-1999.
 PD
 XX 13-MAR-1998; 98WO-US005039.
 PF
 XX 13-MAR-1998; 98WO-US005039.
 PR
 XX (EPIM-) EPIMMUNE INC.
 PA
 PI Sette A, Kubo RT, Sidney J, Cellis E, Grey HM, Southwood S;
 XX WPI; 1999-551214/46.
 DR
 XX New immunogenic peptides with HLA binding motif, useful in treatment and
 PT diagnosis of cancers and viral diseases.
 PT
 XX Claim 1; Page 58; 150pp; English.
 PS
 XX AAY45390 to AAY48214 represent specifically claimed immunogenic peptides
 CC having a human major histocompatibility complex (MHC) Class I (also known
 CC as human leukocyte antigen (HLA)) binding motif. The immunogenic peptides
 CC can bind to a specific HLA allele (i.e. HLA-A subtypes HLA-A2.1, A1, A3.2
 CC or A24.1 or HLA-B or C) and induce a cytotoxic T cell response against
 CC the antigen from which the peptide is derived. Cytotoxic T lymphocytes
 CC (CTLs) which destroy antigen-bearing cells are normally induced by an
 CC antigen in the form of a peptide fragment bound to a HLA molecule, rather
 CC than the intact foreign antigen itself, and are particularly important in
 CC tumour rejection and in fighting viral infections. The peptides are
 CC therefore useful therapeutically to treat or prevent viral infections and
 CC cancers in mammals (especially humans) e.g. prostate cancer, hepatitis B
 CC and C, AIDS, and renal carcinoma. They can be administered as vaccines to
 CC elicit an immune response in individuals susceptible or otherwise at risk
 CC of viral infection or cancer, or used to treat chronic or acute
 CC conditions. They are also useful diagnostically, and can be used to
 CC induce a cytotoxic T cell response, by contacting a cytotoxic T cell with
 CC the peptide e.g. to produce CTLs ex vivo for infusion back into a
 CC patient. The polynucleotides encoding the immunogenic peptides are also
 CC useful therapeutically and for immunisation as above

Sequence 9 AA;

Query Match 62.7%; Score 32; DB 2; Length 9;
 Best Local Similarity 71.4%; Pred. No. 1.8e+06;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;


```

Qy      2 LYDGMH 8
Db      3 YDGMH 9

RESULT 14
ID      AAY46090
XX      AAY46090 standard; peptide; 9 AA.
AC      AAY46090;
XX      01-DEC-1999 (first entry)
XX      Immunogenic peptide having a human leukocyte antigen binding motif #701.
DE      Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
KW      immune response; T cell activation; major histocompatibility complex;
KW      cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
KW      prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
KW      vaccine; immunisation.
XX      Synthetic.
OS      Homo sapiens.
XX      WO9945954-A1.
XX      16-SEP-1999.
XX      13-MAR-1998; 98WO-US005039.
XX      13-MAR-1998; 98WO-US005039.
XX      (EPIM-) EPIMMUNE INC.
PI      Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;
DR      WPI; 1999-551214/46.
XX      New immunogenic peptides with HLA binding motif, useful in treatment and
PT      diagnosis of cancers and viral diseases.
XX      Claim 1; Page 56; 150pp; English.
XX      AAY45390 to AAY48214 represent specifically claimed immunogenic peptides
CC      having a human major histocompatibility complex (MHC) Class I (also known
CC      as human leukocyte antigen (HLA)) binding motif. The immunogenic peptides
CC      can bind to a specific HLA allele (i.e. HLA-A subtypes HLA-A2.1, A1, A3.2
CC      or A24.1 or HLA-B or C) and induce a cytotoxic T cell response against
CC      the antigen from which the peptide is derived. Cytotoxic T lymphocytes
CC      (CTLs) which destroy antigen-bearing cells are normally induced by an
CC      antigen in the form of a peptide fragment bound to a HLA molecule, rather
CC      than the intact foreign antigen itself, and are particularly important in
CC      tumour rejection and in fighting viral infections. The peptides are
CC      therefore useful therapeutically to treat or prevent viral infections and
CC      cancers in mammals (especially humans) e.g. prostate cancer, hepatitis B
CC      and C, AIDS, and renal carcinoma. They can be administered as vaccines to
CC      elicit an immune response in individuals susceptible or otherwise at risk
CC      of viral infection or cancer, or used to treat chronic or acute
CC      conditions. They are also useful diagnostically, and can be used to
CC      induce a cytotoxic T cell response, by contacting a cytotoxic T cell with
CC      the peptide e.g. to produce CTLs ex vivo for infusion back into a
CC      patient. The polynucleotides encoding the immunogenic peptides are also
CC      useful therapeutically and for immunisation as above
XX      Sequence 9 AA;
SQ      Query Match 60.8%; Score 31; DB 2; Length 9;
        Best Local Similarity 83.3%; Pred. No. 1.8e+06;
        Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy      3 YDGMH 8
Db      3 YDGMH 9

RESULT 15
ID      AAY46489
XX      AAY46489 standard; peptide; 9 AA.
AC      AAY46489;
XX      01-DEC-1999 (first entry)
XX      Immunogenic peptide having a human leukocyte antigen binding motif #1100.
DE      Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
KW      immune response; T cell activation; major histocompatibility complex;
KW      cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
KW      prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
KW      vaccine; immunisation.
XX      Synthetic.
OS      Homo sapiens.
XX      WO9945954-A1.
XX      16-SEP-1999.
XX      13-MAR-1998; 98WO-US005039.
XX      13-MAR-1998; 98WO-US005039.
XX      (EPIM-) EPIMMUNE INC.
PI      Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;
DR      WPI; 1999-551214/46.
XX      New immunogenic peptides with HLA binding motif, useful in treatment and
PT      diagnosis of cancers and viral diseases.
XX      Claim 1; Page 74; 150pp; English.
XX      AAY45390 to AAY48214 represent specifically claimed immunogenic peptides
CC      having a human major histocompatibility complex (MHC) Class I (also known
CC      as human leukocyte antigen (HLA)) binding motif. The immunogenic peptides
CC      can bind to a specific HLA allele (i.e. HLA-A subtypes HLA-A2.1, A1, A3.2
CC      or A24.1 or HLA-B or C) and induce a cytotoxic T cell response against
CC      the antigen from which the peptide is derived. Cytotoxic T lymphocytes
CC      (CTLs) which destroy antigen-bearing cells are normally induced by an
CC      antigen in the form of a peptide fragment bound to a HLA molecule, rather
CC      than the intact foreign antigen itself, and are particularly important in
CC      tumour rejection and in fighting viral infections. The peptides are
CC      therefore useful therapeutically to treat or prevent viral infections and
CC      cancers in mammals (especially humans) e.g. prostate cancer, hepatitis B
CC      and C, AIDS, and renal carcinoma. They can be administered as vaccines to
CC      elicit an immune response in individuals susceptible or otherwise at risk
CC      of viral infection or cancer, or used to treat chronic or acute
CC      conditions. They are also useful diagnostically, and can be used to
CC      induce a cytotoxic T cell response, by contacting a cytotoxic T cell with
CC      the peptide e.g. to produce CTLs ex vivo for infusion back into a
CC      patient. The polynucleotides encoding the immunogenic peptides are also
CC      useful therapeutically and for immunisation as above
XX      Sequence 9 AA;
SQ      Query Match 54.9%; Score 28; DB 2; Length 9;
        Best Local Similarity 100.0%; Pred. No. 1.8e+06;
        Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      5 GMEHL 9
Db      5 GMEHL 9

```

Search completed: November 15, 2005, 15:52:31
Job time : 164 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 15, 2005, 15:44:54 ; Search time 38 Seconds
(without alignments)

22.788 Million cell updates/sec

Title: US-09-856-812B-42

Perfect score: 51

Sequence: 1 GLYDGMHL 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 791

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_79:*

1: PIR1.*

2: PIR2.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	37.3	9	2 S10784	enamelin i - bovin
2	18	35.3	9	2 E28854	fibrinopeptide B -
3	18	35.3	9	2 F28854	fibrinopeptide B -
4	18	35.3	9	2 P0002	chlorophyll a/b-bi
5	18	35.3	9	2 A37027	macrophage chemota
6	17	33.3	7	2 A11483	aspartate transami
7	17	33.3	9	2 D28854	fibrinopeptide B -
8	17	33.3	9	2 P50253	glycine cleavage s
9	16	31.4	8	2 A28719	thymic humoral fac
10	15	29.4	6	2 PC4392	whey glycoprotein
11	15	29.4	9	2 S70334	endosperm protein,
12	15	29.4	9	2 P70225	Ig heavy chain CDR
13	15	29.4	9	2 A56029	N-methylpurine DNA
14	14	27.5	4	2 P70240	Ig heavy chain CDR
15	14	27.5	6	2 JN0861	peptidyl-di-peptida
16	14	27.5	6	2 P70589	T-cell receptor be
17	14	27.5	8	2 T14906	hypothetical prote
18	14	27.5	8	2 B33099	158K exoantigen -
19	14	27.5	8	2 P70725	T-cell receptor be
20	14	27.5	8	2 XGHUEU	urine glycopeptide
21	13.5	26.5	8	2 E47393	neuroglycinamide
22	13	25.5	7	2 A12016	formylglycinamide
23	13	25.5	8	2 PA0032	protein QA300040 -
24	13	25.5	8	2 PNO043	phosphatidylethano
25	13	25.5	8	2 S11078	glucose-6-phosphat
26	13	25.5	8	2 P70030	inulinase (EC 3.2.
27	13	25.5	8	2 E60588	sperm-activating p
28	13	25.5	8	2 G60588	sperm-activating p
29	13	25.5	9	2 C24180	fibrinogen beta ch

30 13 25.5 9 2 PT0270 Ig heavy chain CRD
31 13 25.5 9 2 S36850 Ig heavy chain v r
32 13 25.5 9 2 PH0108 late G1-69 protein
33 13 25.5 9 2 B39841 dextranucrase (EC
34 12 23.5 4 2 A48360 gamma subunit of p
35 12 23.5 4 2 PT0271 Ig heavy chain CRD
36 12 23.5 5 2 B61445 leu-enkephalin - b
37 12 23.5 5 2 A61445 Met-enkephalin - b
38 12 23.5 5 2 PT0699 T-cell receptor be
39 12 23.5 5 2 PT0703 T-cell receptor be
40 12 23.5 5 2 I40598 biotin B - Citroba
41 12 23.5 6 2 PT0519 T-cell receptor be
42 12 23.5 6 2 PT0604 T-cell receptor be
43 12 23.5 6 2 PT0657 T-cell receptor be
44 12 23.5 6 2 PT0720 T-cell receptor be
45 12 23.5 7 2 A60224 Met-enkephalin-Arg

ALIGNMENTS

RESULT 1

S10784

enamelin i - bovine (fragment)

C:Species: Bos primigenius taurus (cattle)

C>Date: 19-Mar-1997 #sequence_revision 21-Nov-1998 #text_change 09-Jul-2004

C:Accession: S10784

R:Strawich, E.; Glincher, M.J.

R:J. Biochem. 191, 47-56, 1990

A>Title: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelin' is also

A:Reference number: S10780; MUID:90336641; PMID:2379503

A:Accession: S10784

A:Molecule type: protein

A:Residues: 1-9 <STR>

A:Cross-references: UNIPROT:Q7M2M7

C:Keywords: enamel; phosphoprotein

Query Match 37.3%; Score 19; DB 2; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 YDG 5

Db 3 YDG 5

RESULT 2

E28854

fibrinopeptide B - hamadryas baboon

C:Species: Papio hamadryas (hamadryas baboon)

C>Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 09-Jul-2004

C:Accession: E28854

R:Nakamura, S.; Takenaka, O.; Takahashi, K.

J. Biochem. 94, 1973-1978, 1983

A>Title: Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas, and Theropit

A:Reference number: A91973; MUID:84161822; PMID:6423621

A:Accession: E28854

A:Molecule type: protein

A:Residues: 1-9 <NAK>

A:Cross-references: UNIPROT:P19343

C:Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulf

Query Match 35.3%; Score 18; DB 2; Length 9;

Best Local Similarity 60.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLYDG 5

Db 4 GLPHG 8

RESULT 3

F28854

fibrinopeptide B - gelada baboon
 C;Species: Theropithecus gelada (gelada baboon)
 C;Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 09-Jul-2004
 C;Accession: F28854
 R;Nakamura, S.; Takenaka, O.; Takahashi, K.
 J. Biochem. 94, 1973-1978, 1983
 A;Title: Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas, and Theropithecus gelada)
 A;Reference number: A91973; MUID:84161822; PMID:6423621
 A;Accession: F28854
 A;Molecule type: protein
 A;Residues: 1-9 <NAK>
 A;Cross-references: UNIPROT:P19342
 C;Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfide

Query Match 35.3%; Score 18; DB 2; Length 9;
 Best Local Similarity 60.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLYDG 5
 ||:|
 Db 4 GLFGG 8

RESULT 4

PW0002
 chlorophyll a/b-binding protein 31K - green alga (Dunaliella tertiolecta) (fragment)
 N;Alternate names: photosystem II light-harvesting chlorophyll 31K protein
 C;Species: Dunaliella tertiolecta
 C;Date: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 24-Nov-1999
 C;Accession: PW0002
 R;LaRoche, J.; Bennett, J.; Falkowski, P.G.
 Gene 95, 165-171, 1990
 A;Title: Characterization of a cDNA encoding for the 28.5-kDa LHCII apoprotein from the green alga Dunaliella tertiolecta
 A;Reference number: JMW040; MUID:91065528; PMID:2249775
 A;Accession: PW0002
 A;Molecule type: protein
 A;Residues: 1-9 <LAR>
 C;Superfamily: chlorophyll a/b-binding protein
 C;Keywords: chloroplast; grana; light-harvesting complex; membrane adhesion; membrane protein

Query Match 35.3%; Score 18; DB 2; Length 9;
 Best Local Similarity 60.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 YDGME 7
 ||:|
 Db 3 YDEMQ 7

RESULT 5

A37027
 macrophage chemotactic factor - human (fragment)
 N;Alternate names: T-cell hybridoma D6-18 protein
 C;Species: Homo sapiens (man)
 C;Date: 31-Jan-1992 #sequence_revision 31-Jan-1992 #text_change 09-Jul-2004
 C;Accession: A37027
 R;Yoshizuka, N.; Yoshimura, M.; Tsuchiya, S.; Okamoto, K.; Kobayashi, Y.; Osawa, T.
 Cell. Immunol. 123, 212-225, 1989
 A;Title: Macrophage chemotactic factor (MCF) produced by a human T cell hybridoma clone.
 A;Reference number: A37027; MUID:89376581; PMID:2505934
 A;Accession: A37027
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-9 <YOS>
 A;Cross-references: UNIPROT:Q7M4S2

Query Match 35.3%; Score 18; DB 2; Length 9;
 Best Local Similarity 57.1%; Pred. No. 2.8e+05;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GLYDGM 7
 ||:|
 Db 3 GRZDGE 9

RESULT 6

A11483
 aspartate transaminase (EC 2.6.1.1), mitochondrial - sheep (fragment)
 N;Alternate names: aspartate aminotransferase, mitochondrial
 C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 20-Aug-1999
 C;Accession: A11483
 R;Campos-Cavieles, M.; Milstein, C.P.
 Biochem. J. 147, 275-281, 1975
 A;Title: The sequences of the coenzyme-binding peptide in the cytoplasmic and the mitochondrial aspartate transaminase from sheep
 A;Reference number: A11483; MUID:76039441; PMID:1180894
 A;Accession: A11483
 A;Molecule type: protein
 A;Residues: 1-7 <CAM>
 A;Experimental source: liver
 C;Keywords: aminotransferase; mitochondrion; phosphoprotein; pyridoxal phosphate
 P;2/Binding site: pyridoxal phosphate (Lys) (covalent) #status experimental

Query Match 33.3%; Score 17; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLY 3
 ||:|
 Db 5 GLY 7

RESULT 7

D28854
 fibrinopeptide B - olive baboon
 C;Species: Papio anubis, Papio hamadryas anubis (olive baboon)
 C;Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 09-Jul-2004
 C;Accession: D28854
 R;Nakamura, S.; Takenaka, O.; Takahashi, K.
 J. Biochem. 94, 1973-1978, 1983
 A;Title: Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas, and Theropithecus gelada)
 A;Reference number: A91973; MUID:84161822; PMID:6423621
 A;Accession: D28854
 A;Molecule type: protein
 A;Residues: 1-9 <NAK>
 A;Cross-references: UNIPROT:P19344
 C;Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfide

Query Match 33.3%; Score 17; DB 2; Length 9;
 Best Local Similarity 60.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLYDG 5
 ||:|
 Db 4 GLFRG 8

RESULT 8

PS0253
 glycine cleavage system protein H - rice (strain Nihonbare) (fragment)
 N;Alternate names: glycine decarboxylase complex H protein
 C;Species: Oryza sativa (rice)
 C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
 C;Accession: PS0253
 R;Tsugita, A.
 submitted to JIPID, April 1993
 A;Reference number: PS0206
 A;Accession: PS0253
 A;Molecule type: protein
 A;Residues: 1-9 <TSU>
 A;Cross-references: UNIPROT:Q7M1V3

Query Match 33.3%; Score 17; DB 2; Length 9;
 Best Local Similarity 40.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 DGMH 8
|:|
Db 5 DGLKY 9

RESULT 9

A28719
thymic humoral factor gamma-2 - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
C;Accession: A28719
R;Burststein, Y.; Buchner, V.; Pecht, M.; Trainin, N.
Biochemistry 27, 4066-4071, 1988
A;Title: Thymic humoral factor gamma-2: purification and amino acid sequence of an immunoreactive protein
A;Reference number: A28719; MUID:98326920; PMID:3261994
A;Accession: A28719
A;Molecule type: protein
A;Residues: 1-8 <BUR>
A;Cross-references: UNIPROT:O18787

Query Match 31.4%; Score 16; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 LYDGMH 9
|:|:|
Db 1 LEDGPKFL 8

RESULT 10

PC4392
whey glycoprotein WGP-88 - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 10-Nov-1997 #sequence_revision 10-Nov-1997 #text_change 07-May-1999
C;Accession: PC4392
R;Hwangbo, S.; Azuma, N.; Kurisaki, J.; Kanno, C.
Biosci. Biotechnol. Biochem. 61, 1568-1574, 1997
A;Title: Purification and characterization of novel whey glycoprotein WGP-88 which binds to the monoclonal antibody to PAS-4 glycoprotein.
A;Reference number: PC4392; MUID:97480944; PMID:9339560
A;Accession: PC4392
A;Molecule type: protein
A;Residues: 1-6 <HWA>
A;Experimental source: milk
C;Comment: This protein binds to the monoclonal antibody to PAS-4 glycoprotein.

Query Match 29.4%; Score 15; DB 2; Length 6;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 DGMH 7
|:|
Db 1 DGVO 4

RESULT 11

S70334
endosperm protein, 45K - rye (fragment)
C;Species: Secale cereale (rye)
C;Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 17-Apr-1998
C;Accession: S70334
R;Roche, A.; Calero, M.; Soriano, F.; Mendez, E.
Biochim. Biophys. Acta 1295, 13-22, 1996
A;Title: Identification of major rye secalins as coeliac immunoreactive proteins.
A;Reference number: S70327; MUID:96283789; PMID:8679669
A;Accession: S70334
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-9 <ROC>

Query Match 29.4%; Score 15; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 YDG 5
|:|
Db 7 YEG 9

RESULT 12

PT0225
Ig heavy chain CDR3 region (clone 1-103) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0225
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and junctional diversity in the CDR3 region of a human anti-lymphoma monoclonal antibody
A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0225
A;Molecule type: DNA
A;Residues: 1-9 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

Query Match 29.4%; Score 15; DB 2; Length 9;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 LYDGM 6
|:|
Db 2 MFGGM 6

RESULT 13

A56029
N-methylpurine DNA glycosylase - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 09-Jul-2004
C;Accession: A56029
R;Roy, R.; Brooks, C.; Mitra, S.
Biochemistry 33, 15131-15140, 1994
A;Title: Purification and biochemical characterization of recombinant N-methylpurine-DNA glycosylase from mouse
A;Reference number: A56029; MUID:95092772; PMID:7999773
A;Accession: A56029
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-9 <ROY>
A;Cross-references: UNIPROT:Q7M0H1

Query Match 29.4%; Score 15; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 MEH 8
|:|
Db 1 MDH 3

RESULT 14

PT0240
Ig heavy chain CDR3 region (clone 2-100B) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0240
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and junctional diversity in the CDR3 region of a human anti-lymphoma monoclonal antibody
A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0240
A;Molecule type: DNA
A;Residues: 1-4 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

Query Match 27.5%; Score 14; DB 2; Length 4;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 YDGM 6
| |
Db 1 YPGL 4

RESULT 15

JN0861

peptidyl-di-peptidase A inhibitory peptide C111 - striped bonito

C;Species: Sarda orientalis (striped bonito)

C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 07-May-1999

C;Accession: JN0861

R;Matsumura, N.; Fujii, M.; Takeda, Y.; Shimizu, T.

Biosci. Biotechnol. Biochem. 57, 1743-1744, 1993

A;Title: Isolation and characterization of angiotensin I-converting enzyme inhibitory pe

A;Reference number: JN0859; MUID:94080036; PMID:7764272

A;Accession: JN0861

A;Molecule type: protein

A;Residues: 1-6 <MAT>

A;Experimental source: liver

C;Comment: The carboxyl end is essential for the protein's expression of angiotensin I-c

C;Superfamily: bradykinin-potentiating peptide

C;Keywords: angiotensin-converting enzyme inhibitor

Query Match 27.5%; Score 14; DB 2; Length 6;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLY 3
| |
Db 1 GYV 3

Search completed: November 15, 2005, 15:56:13

Job time : 40 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 15, 2005, 15:43:59 ; Search time 172 Seconds
(without alignments)
26.795 Million cell updates/sec

Title: US-09-856-812B-42
Perfect score: 51
Sequence: 1 GLYDGMHL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1455

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_03:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	43.1	8	2 Q9P285	Q9P285 homo sapien
2	20	39.2	9	2 Q9XSL0	Q9XSL0 capra hircu
3	19	37.3	9	2 Q7M2M7	Q7M2M7 bos taurus
4	18	35.3	9	1 FIBB_PAPHA	F19343 papio hamad
5	18	35.3	9	1 FIBB_THEGE	F19342 theropithec
6	18	35.3	9	2 Q7M4S2	Q7M4S2 homo sapien
7	17	33.3	8	1 DYS1_LIMIN	P82079 limodynast
8	17	33.3	8	2 Q70Y68	Q70Y68 prostanther
9	17	33.3	9	1 FIBB_PAPAN	F19344 papio anubi
10	17	33.3	9	2 Q70YA2	Q70YA2 alvesia ros
11	17	33.3	9	2 Q7MLV3	Q7MLV3 oryza sativ
12	16	31.4	9	2 Q712A6	Q712A6 sinorhizobi
13	15	29.4	7	1 ALL7_CYPDPO	P82158 cydia pomon
14	15	29.4	8	2 Q9TWH6	Q9TWH6 perineris
15	15	29.4	8	2 P83158	P83158 anabaena sp
16	15	29.4	9	1 NSK1_SABBU	P41492 sarcophaga
17	15	29.4	9	1 RE42_LITRU	P82075 litoria rub
18	15	29.4	9	2 Q70SM2	Q70SM2 homo sapien
19	15	29.4	9	2 Q67AQ7	Q67AQ7 homo sapien
20	15	29.4	9	2 Q7MOH1	Q7MOH1 mus musculu
21	14	27.5	7	1 MNP1_LEPDE	P42984 leptinotars
22	14	27.5	7	2 Q991B2	Q991B2 gnatholebia
23	14	27.5	8	1 GLUR_HUMAN	P02729 homo sapien
24	14	27.5	8	2 Q80H91	Q80H91 newcastle d
25	14	27.5	9	2 Q7S182	Q7S182 neurospora
26	14	27.5	9	2 Q67AR4	Q67AR4 homo sapien
27	14	27.5	9	2 Q67AR6	Q67AR6 homo sapien
28	14	27.5	9	2 Q67AR7	Q67AR7 homo sapien
29	14	27.5	9	2 Q67AT1	Q67AT1 homo sapien
30	14	27.5	9	2 Q67AT2	Q67AT2 homo sapien
31	14	27.5	9	2 Q937H9	Q937H9 enterobacte

32 14 27.5 9 2 Q937J8
33 13.5 26.5 8 1 ALL5_CALVO
34 13 25.5 7 2 Q8KM59
35 13 25.5 7 2 Q8K3H6
36 13 25.5 8 1 ALL5_CYDPO
37 13 25.5 8 1 FUS6_FUSSO
38 13 25.5 8 2 Q7M4U4
39 13 25.5 8 2 Q6SE42
40 13 25.5 8 2 Q70MX3
41 13 25.5 8 2 Q7M4C6
42 13 25.5 8 2 Q7M4C7
43 13 25.5 8 2 Q9XSY1
44 13 25.5 8 2 P92211
45 13 25.5 8 2 P92215

ALIGNMENTS

RESULT 1
Q9P285 PRELIMINARY; PRT; 8 AA.
AC Q9P285;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE Clotting factor VIII (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Shibata M., Shima M., Morichika S., Yoshioka A.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB040872; BAA94312.1; -;
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 866 MW; 1C16987AAB05BDD3 CRC64;

Query Match 43.1%; Score 22; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DGM6 7
DB 5 DGM6 8

RESULT 2
Q9XSL0 PRELIMINARY; PRT; 9 AA.
AC Q9XSL0;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Alpha s2-casein (Fragment).
GN Names-csn1s2;
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=21313038; PubMed=11419340;
RA Ramunno L., Longobardi E., Pappalardo M., Rando A., Di Gregorio P.,
RA Cosenza G., Mariani P., Pastore N., Masina P.;
RT "An allele associated with a non detectable amount of as2 casein in
goat milk.";
RL Anim. Genet. 32:19-26(2001).
DR EMBL; AJ238475; CAB44298.1; -.

```

FT NON TER 1 1 alpha s2-casein.
FT CHAIN <1 >9
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1047 MW; AAA2A5A5B051EB16 CRC64;

Query Match
Best Local Similarity 39.2%; Score 20; DB 2; Length 9;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 MEHL 9
Db |||:
2 MEHI 5

RESULT 3
Q7M2M7 PRELIMINARY; PRT; 9 AA.
AC Q7M2M7;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Enamelin 1 (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=90336641; PubMed=2379503;
RA Strawich E., Glimcher M.J.;
RT "Tooth 'enamelins' identified mainly as serum proteins. Major
FT 'enamelin' is albumin.";
RL Eur. J. Biochem. 191:47-56(1990).
DR PIR; S10784; S10784.
FT NON TER 1 1
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1036 MW; 2D867DD9C87ABB47 CRC64;

Query Match
Best Local Similarity 37.3%; Score 19; DB 2; Length 9;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 YDG 5
Db |||:
3 YDG 5

RESULT 4
FIBB PAFPA
ID_FIBB PAFPA STANDARD; PRT; 9 AA.
AC P19343;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN Name=FGB;
OS Papio hamadryas (Hamadryas baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Papio.
OX NCBI_TaxID=9557;
RN [1]
RP SEQUENCE.
RX MEDLINE=84161822; PubMed=6423621;
RA Nakamura S., Takenaka O., Takahashi K.;
RT "Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas,
RT and Theropithecus gelada): their amino acid sequences and evolutionary
RL rates and a molecular phylogeny for the baboons.";
RL J. Biochem. 94:1973-1978(1983).
CC -1- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC polymerize into fibrin and acting as a cofactor in platelet
CC aggregation.
CC -1- SUBUNIT: Hexamer containing 2 sets of 3 nonidentical chains
CC (alpha, beta and gamma), linked to each other by disulfide bonds.
CC -1- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC which cleaves fibrinopeptides A and B from alpha and beta chains,
CC and thus exposes the N-terminal polymerization sites responsible
CC for the formation of the soft clot.
DR PIR; F28854; F28854.
DR InterPro: IPR002181; Fibrinogen C.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
KW Blood coagulation; Direct protein sequencing; Plasma.
FT P2PTIDE 1 9 Fibrinopeptide B.
FT NON TER 9 9
SQ SEQUENCE 9 AA; 977 MW; DDFE7879C7287B06 CRC64;

Query Match
Best Local Similarity 35.3%; Score 18; DB 1; Length 9;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLYDG 5
Db |||:
4 GLFGG 8

RESULT 6
Q7M4S2

```

```

CC -1- SUBUNIT: Hexamer containing 2 sets of 3 nonidentical chains
CC (alpha, beta and gamma), linked to each other by disulfide bonds.
CC -1- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC which cleaves fibrinopeptides A and B from alpha and beta chains,
CC and thus exposes the N-terminal polymerization sites responsible
CC for the formation of the soft clot.
DR PIR; E28854; E28854.
DR InterPro: IPR002181; Fibrinogen C.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
KW Blood coagulation; Direct protein sequencing; Plasma.
FT P2PTIDE 1 9 Fibrinopeptide B.
FT NON TER 9 9
SQ SEQUENCE 9 AA; 1057 MW; DDFE71B9C7287B06 CRC64;

Query Match
Best Local Similarity 35.3%; Score 18; DB 1; Length 9;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLYDG 5
Db |||:
4 GLFGG 8

RESULT 5
FIBB THEGE
ID_FIBB THEGE STANDARD; PRT; 9 AA.
AC P19342;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN Name=FGB;
OS Theropithecus gelada (Gelada baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Theropithecus.
OX NCBI_TaxID=9565;
RN [1]
RP SEQUENCE.
RX MEDLINE=84161822; PubMed=6423621;
RA Nakamura S., Takenaka O., Takahashi K.;
RT "Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas,
RT and Theropithecus gelada): their amino acid sequences and evolutionary
RL rates and a molecular phylogeny for the baboons.";
RL J. Biochem. 94:1973-1978(1983).
CC -1- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC polymerize into fibrin and acting as a cofactor in platelet
CC aggregation.
CC -1- SUBUNIT: Hexamer containing 2 sets of 3 nonidentical chains
CC (alpha, beta and gamma), linked to each other by disulfide bonds.
CC -1- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC which cleaves fibrinopeptides A and B from alpha and beta chains,
CC and thus exposes the N-terminal polymerization sites responsible
CC for the formation of the soft clot.
DR PIR; F28854; F28854.
DR InterPro: IPR002181; Fibrinogen C.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
KW Blood coagulation; Direct protein sequencing; Plasma.
FT P2PTIDE 1 9 Fibrinopeptide B.
FT NON TER 9 9
SQ SEQUENCE 9 AA; 977 MW; DDFE7879C7287B06 CRC64;

Query Match
Best Local Similarity 35.3%; Score 18; DB 1; Length 9;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLYDG 5
Db |||:
4 GLFGG 8

RESULT 6
Q7M4S2

```


ID Q7M4S2 PRELIMINARY; PRT; 9 AA.
 AC Q7M4S2;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Macrophage chemotactic factor (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=89376581; PubMed=2505934;
 RA Yoshizuka N., Yoshimura M., Tsuchiya S., Okamoto K., Kobayashi Y.,
 RA Osawa T.;
 RT "Macrophage chemotactic factor (MCP) produced by a human T cell
 RT hybridoma clone";
 RL Cell. Immunol. 123:212-225(1989).
 DR PIR; A37027; A37027.
 FT NON_TER 1
 FT NON_TER 9
 SQ SEQUENCE 9 AA; 1048 MW; 44CEB87AB9940877 CRC64;

 Query Match 35.3%; Score 18; DB 2; Length 9;
 Best Local Similarity 57.1%; Pred. No. 1.6e+06;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

 QY 1 GLYDGM 7
 Db | | | | |
 3 GRZDGE 9

 RESULT 7
 DVS1 LIMIN STANDARD; PRT; 8 AA.
 AC P82079;
 DT 29-MAR-2004 (Rel. 43, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Dynastin 1.
 OS Limnodynastes interioris (Giant banjo frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hylaidea; Myobatrachidae;
 OC Limnodynastinae; Limnodynastes.
 OX NCBI_TaxID=30362;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Tibial Gland;
 RA Raftery M.J., Bradford A.M., Bowie J.H., Wallace J.C., Tyler M.J.;
 RT "Peptides from Australian frogs. The structure of the dynastins from
 RT the banjo frogs Limnodynastes interioris, Limnodynastes dumerilii and
 RT Limnodynastes terraereginae";
 RL Aust. J. Chem. 46:833-842(1993).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Skin.
 CC -1- MASS SPECTROMETRY: MW=729; METHOD=FAB; RANGE=1-8; NOTE=Ref.1.
 KW Direct protein sequencing.
 SQ SEQUENCE 8 AA; 729 MW; 7C28772865B72728 CRC64;

 Query Match 33.3%; Score 17; DB 1; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1.6e+06;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

 QY 1 GLYDGM 6
 Db | | | | |
 1 GLLSGL 6

 RESULT 8
 Q70V68
 ID Q70Y68 PRELIMINARY; PRT; 8 AA.
 AC Q70Y68;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Ribosomal protein (Fragment).
 GN Name=rp16;
 OS Prostanthera nivea (snowy mintbush).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asteride;
 OC Lamiales; Lamiales; Lamiaceae; Prostantheroideae; Westringieae;
 OC Prostanthera.
 OX NCBI_TaxID=38863;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=15019625; DOI=10.1016/j.ympev.2003.08.002;
 RA Paton A., Springate D.A., Siddle S., O'Brien D., Grayer R., Harley M.M.,
 RA Willis F., Simonds M.S.J., Powell M.P., Savolainen V.;
 RT "Phylogeny and evolution of basils and allies (Ocimeae, Labiatae)
 RT based on three plastid DNA regions";
 RL Mol. Phylogenet. Evol. 31:277-299(2004).
 DR EMBL; AJ505403; CAD45523.1; -.
 DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
 KW Ribosomal protein.
 FT NON_TER 1
 FT NON_TER 8
 SQ SEQUENCE 8 AA; 838 MW; C821F2C058786415 CRC64;

 Query Match 33.3%; Score 17; DB 2; Length 8;
 Best Local Similarity 60.0%; Pred. No. 1.6e+06;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

 QY 5 GMEHL 9
 Db | | | | |
 4 GIVHL 8

 RESULT 9
 FIBB PAPAN STANDARD; PRT; 9 AA.
 AC P19344;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
 GN Name=FGB;
 OS Papio anubis (Olive baboon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
 OC Cercopithecinae; Papio.
 OX NCBI_TaxID=9555;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=84161822; PubMed=6423621;
 RA Nakamura S., Takenaka O., Takahashi K.;
 RT "Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas,
 RT and Theropithecus gelada): their amino acid sequences and evolutionary
 RT rates and a molecular phylogeny for the baboons";
 RL J. Biochem. 94:1973-1978(1983).
 CC -1- FUNCTION: Fibrinogen has a double function: yielding monomers that
 CC polymerize into fibrin and acting as a cofactor in platelet
 CC aggregation.
 CC -1- SUBUNIT: Hexamer containing 2 sets of 3 nonidentical chains
 CC (alpha, beta and gamma), linked to each other by disulfide bonds.
 CC -1- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
 CC which cleaves fibrinopeptides A and B from alpha and beta chains,
 CC and thus exposes the N-terminal polymerization sites responsible
 CC for the formation of the soft clot.
 DR PIR; D28854; D28854.
 DR InterPro; IPR002181; Fibrinogen C.
 DR PROSITE; PS00514; FIBRIN AG C DOMAIN; PARTIAL.
 KW Blood coagulation; Direct protein sequencing; Plasma.
 FT PEPTIDE 1 9 Fibrinopeptide B.
 FT NON_TER 9
 SQ SEQUENCE 9 AA; 1076 MW; DDF6409C7287B06 CRC64;

```

Query Match      33.3%; Score 17; DB 1; Length 9;
Best Local Similarity 60.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLYDG 5
Db 4 GLFRG 8

RESULT 10
Q70YA2 PRELIMINARY; PRT; 9 AA.
AC Q70YA2;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DE Ribosomal protein (Fragment).
GN Name=rp16;
OS Alvesia rosmarinifolia.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Lamiaceae; Nepetoideae; Ocimeae; Alvesia.
OX NCBI_TaxID=204103;
RN [1]
RP SEQUENCE FROM N.A.
EX PubMed=15019625; DOI=10.1016/j.ympev.2003.08.002;
RA Paton A., Springate D.A., Sudde S., Otieno D., Grayer R., Harley M.M.,
RA Willis F., Simonds M.S.J., Powell M.F., Savolainen V.;
RT "Phylogeny and evolution of basilis and allies (Ocimeae, Labiatae)
RT based on three plastid DNA regions.";
RL Mol. Phylogenet. Evol. 31:277-299(2004).
DR EMBL; AJ505329; CAD45492.1; -.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
KW Ribosomal protein.
FT NON_TER 1
FT NON_TER 9
SQ SEQUENCE 9 AA; 979 MW; 0DF006C5B721F2C0 CRC64;

Query Match      33.3%; Score 17; DB 2; Length 9;
Best Local Similarity 60.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GMEHL 9
Db 1 GIVHL 5

RESULT 11
Q7M1V3 PRELIMINARY; PRT; 9 AA.
AC Q7M1V3;
DT 01-MAR-2004 (TReMBLrel. 26, Created)
DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Glycine cleavage system protein H (Fragment).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartioideae; Oryzaeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE.
RA Teugitla A.;
RL Submitted (APR-1993) to the PIR data bank.
DR PIR; PS0253; PS0253.
DR Gramene; Q7M1V3; -.
FT NON_TER 1
FT NON_TER 9
SQ SEQUENCE 9 AA; 1048 MW; 0BF437287AA732C0 CRC64;

Query Match      33.3%; Score 17; DB 2; Length 9;

Qy 1 GLYDG 5
Db 4 GLFRG 8

RESULT 12
Q712A6 PRELIMINARY; PRT; 9 AA.
AC Q712A6;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DE NodB protein (Fragment).
GN Name=nodB;
OS Sinorhizobium sp. BR816.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxID=142626;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BR816;
RA Chen W.M., Moulin L., Bontemps C., Vandamme P., Bena G.,
RA Boivin-Masson C.;
RT "Symbiotic Nitrogen Fixation by beta-Proteobacter ia is widespread in
RT Nature.";
RL J. Bacteriol. 185:0-0(2003).
DR EMBL; AJ300234; CAC82843.1; -.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1048 MW; 803CB72EBAA721F1 CRC64;

Query Match      31.4%; Score 16; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 MEHL 9
Db 1 MTHL 4

RESULT 13
ALL7 CYDPO STANDARD; PRT; 7 AA.
AC P82158;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cydiaastatin 7.
OS Cydia pomonella (Codling moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Tortricoidae; Tortricidae; Olethreutinae; Cydia.
OX NCBI_TaxID=82600;
RN [1]
RP SEQUENCE.
RC TISSUE=Larva;
RX MEDLINE=98054539; PubMed=9392829; DOI=10.1016/S0196-9781(97)00188-5;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
RA Davey M., East P.D., Thorpe A.;
RT "Lepidopteran peptides of the allatostatin superfamily.";
RL Peptides 18:1301-1309(1997).
CC -I- SIMILARITY: Belongs to the allatostatin family.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD_RES 7
FT MOD_RES 7 Leucine amide.
SQ SEQUENCE 7 AA; 873 MW; 672879CABB569350 CRC64;

Query Match      29.4%; Score 15; DB 1; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.6e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LYD 4

```

Job time : 174 secs

Db 2 MYD 4

RESULT 14
Q9TWH6 PRELIMINARY; PRT; 8 AA.
AC Q9TWH6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE BIOACTIVE peptide P4=PUTATIVE ESOPHAGEAL NEUROREGULATOR.
OS Perinereis vancaurica.
OC Eukaryota; Metazoa; Annelida; Polychaeta; Palpata; Aciculata;
OC Phyllocorida; Nereididae; Perinereis.
OX NCBI_TaxID=6355;
RN [1]
RP SEQUENCE.
RA Takahashi T., Furukawa Y., Muneoka Y., Matsushima O., Ikeda T.,
RA Fujita T., Minakata H., Nomoto K.;
RT "Isolation and characterization of four novel bioactive peptides from
RT a polychaete annelid, Perinereis vancaurica.";
RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
SQ SEQUENCE 8 AA; 989 MW; 954772CAA87B0B59 CRC64;

Query Match 29.4%; Score 15; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.6e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 YDG 5
Db 2 YEG 4

RESULT 15
P83158 PRELIMINARY; PRT; 8 AA.
AC P83158;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Photosystem I iron-sulfur center (Photosystem I subunit VII) (9 kDa
DE polypeptide) (PSI-C) (Fragment).
OS Anabaena sp. (strain L31).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
OX NCBI_TaxID=29412;
RN [1]
RP SEQUENCE.
RA Apte S.K., Uhlemann E., Schmid R., Altendorf K.;
RL Submitted (OCT-2001) to Swiss-Prot.
CC -1- FUNCTION: Apoptein for the iron-sulfur centers FA and FB of the
CC Photosystem I complex.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: THE IRON-SULFUR CENTERS ARE SIMILAR TO THOSE OF
CC 'BACTERIAL-TYPE' 4FE-4S FERREDOXINS.
DR GO; GO:0009522; C:photosystem I; IEA.
DR GO; GO:0015979; P:photosynthesis; IEA.
DR InterPro; IPR001450; 4Fe4S_ferredoxin.
DR PROSITE; PS00198; 4FE4S_FERREDOXIN; PARTIAL.
KW 4Fe-4S; Iron-sulfur; Metal-binding; Photosynthesis; Photosystem I.
FT NON TER 8
SQ SEQUENCE 8 AA; 962 MW; C5BB505322D1A1F5 CRC64;

Query Match 29.4%; Score 15; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.6e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LYD 4
Db 6 IYD 8

THIS PAGE BLANK (USPTO)